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OM protein - protein search, using sw model

Run on: May 20, 2005, 13:22:17 ; Search time 42 Seconds
(without alignments)
1050.419 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHSDPMCLTENFNEQ.....GEAARSCGQGVWSQKVVV 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3043	100.0	591	4	US-09-643-657-3
2	2610.5	85.8	633	2	US-08-736-770-3
3	1966.5	64.6	605	4	US-09-949-016-8823
4	1958.5	64.4	592	2	US-08-736-770-6
5	1958.5	64.4	592	4	US-09-702-705-1809
6	1958.5	64.4	592	4	US-09-736-457-1809
7	1958.5	64.4	592	4	US-09-643-657-4
8	1958.5	64.4	592	4	US-09-671-325-1809
9	1897	62.3	591	2	US-08-736-770-5
10	1897	62.3	591	4	US-09-643-657-5
11	1881	61.8	608	2	US-08-736-770-1
12	1832.5	60.2	583	4	US-09-949-016-8267
13	1765.5	58.0	589	4	US-09-643-657-14
14	1757.5	57.8	591	4	US-09-643-657-15
15	1459.5	48.0	620	4	US-09-643-657-13
16	932.5	30.6	573	4	US-09-643-657-18
17	526	17.3	147	4	US-09-370-838-99
18	526	17.3	147	4	US-09-854-133-99
19	509	16.7	159	4	US-09-370-838-98
20	509	16.7	159	4	US-09-854-133-98
21	392	12.9	96	4	US-09-513-999C-5037
22	296	9.7	103	4	US-09-643-657-16
23	239	7.9	64	4	US-09-643-657-17
24	203	6.7	57	4	US-09-621-976-4483
25	197	6.5	573	4	US-09-270-767-44491
26	154.5	5.1	1427	4	US-09-538-092-1044
27	151	5.0	1180	4	US-09-543-681A-6436

28	148	4.9	710	4	US-09-107-532A-5067	Sequence 5067, Ap
29	148	4.9	1288	4	US-09-919-039-209	Sequence 209, Ap
30	146.5	4.8	1531	4	US-09-418-710-29	Sequence 29, Appl
31	146.5	4.8	1531	4	US-09-839-479-29	Sequence 29, Appl
32	145.5	4.8	568	4	US-09-949-016-10580	Sequence 10580, A
33	144	4.7	1857	4	US-09-917-254-91	Sequence 91, Appl
34	144	4.7	1972	4	US-09-538-092-1084	Sequence 1084, Ap
35	144	4.7	1984	4	US-09-949-016-7111	Sequence 7111, Ap
36	144	4.7	1984	4	US-09-949-016-7112	Sequence 7112, Ap
37	144	4.7	1984	4	US-09-949-016-7113	Sequence 7113, Ap
38	142	4.7	1972	4	US-08-875-435B-4	Sequence 4, Appl
39	141.5	4.7	1527	4	US-09-418-710-27	Sequence 27, Appl
40	141.5	4.7	1527	4	US-09-839-479-27	Sequence 27, Appl
41	140.5	4.6	897	1	US-08-095-737-4	Sequence 4, Appl
42	140.5	4.6	897	1	US-08-480-145-4	Sequence 4, Appl
43	140.5	4.6	897	2	US-08-477-389-4	Sequence 4, Appl
44	140.5	4.6	1540	4	US-09-949-016-7037	Sequence 7037, Ap
45	140.5	4.6	2107	4	US-09-949-016-7646	Sequence 7646, Ap

ALIGNMENTS

RESULT 1

US-09-643-657-3

; Sequence 3, Application US/09643657

; Patent No. 6642024

; GENERAL INFORMATION:

; APPLICANT: Diane Pennica

; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/643,657

; FILING DATE: 17-Aug-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/015,089A

; FILING DATE: 29-Jan-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: P1056

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1896

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 591 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-643-657-3

Query Match 100.0%; Score 3043; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.7e-254;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHSDPMCLTENFNEQKVNQAELEISAITQPVVVAIVGLYRTGKSYLKNKLAG 60

Db 1 MALEIHSDPMCLTENFNEQKVNQAELEISAITQPVVVAIVGLYRTGKSYLKNKLAG 60


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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8823
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8823

Query Match      64.4%; Score 1966.5; DB 4; Length 605;
Best Local Similarity 69.7%; Pred. No. 2.2e-161;
Matches 389; Conservative 70; Mismatches 88; Indels 11; Gaps 3;

QY 1 MALEIHMSPMCLINFNQKVNQAEALISAITQPVVVVAIVGLYRTGKSYLNNKLAG 60
Db 14 MASEIHMTPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLNNKLAG 73
QY 61 KNGKFSVASTVQSHTKGIWCVPHNPNNHTLVLLDTGLGDKVEKADNNDIQLPALAL 120
Db 74 KKGKFSLSGTVQSHTKGIWCVPHNPNNHTLVLLDTGLGDKVEKADNNDIQLPALAV 133
QY 121 LLSSTFVYNTVTKIDQGAIDLHNVNTELTDLKARNSPD--LDRVEDPADSASFFPDVW 178
Db 134 LLSSTFVYNTVTKIDQGAIDLHNVNTELTDLKARNSPD--LDRVEDPADSASFFPDVW 193
QY 179 TLRFCLGLEIDGQVTPDEYLENSLRPKQSDQVQNFNLRCLCIQKFFPKKCFIDL 238
Db 194 TLRFCLGLEIDGQVTPDEYLENSLRPKQSDQVQNFNLRCLCIQKFFPKKCFIDL 253
QY 239 PAHQKLAQLETLPDDELEPEFVQVADFCVYFNSKTKTLGGGIQVNGPRLESILVLT 298
Db 254 PVHRRKLAQLETLPDDELEPEFVQVADFCVYFNSKTKTLGGGIQVNGPRLESILVLT 313
QY 299 VNAISSGDLPCINAVLAQRENSAAVQKAIHAHYDQMGQKQVQLPMTLOELLDLHRTS 358
Db 314 VNAISSGDLPCINAVLAQRENSAAVQKAIHAHYDQMGQKQVQLPMTLOELLDLHRTS 373
QY 359 EREAIEVFMKNSFKVDQSFQKLETLDDAKNDICRKNLEASSDYCSALLKIDFGPLEE 418
Db 374 EREAIEVFMKNSFKVDQSFQKLETLDDAKNDICRKNLEASSDYCSALLKIDFGPLEE 433
QY 419 AVKQGIYKPGGKGNLFIOKTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQ 478
Db 434 EVKAGIYKPGGKGNLFIOKTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQ 493
QY 479 ALTETEKKKKAQVKAABAKAORLAAIQRONEQMOERERLHQEQVQVQVQVQVQVQV 534
Db 494 TLTEKEKEIEVERVKAESAQASAKMLQEMQKQKERSYQEHKQLTKERMENDRV 553
QY 535 NWLAQQ-----KMQEQQ 547
Db 554 QLLKEQERTLALKLOEQE 571

RESULT 4
US-08-736-770-6
; Sequence 6, Application US/08736770
; Patent No. 5871965
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/736,770
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0145 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 592 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 183002
; US-08-736-770-6

Query Match      64.4%; Score 1958.5; DB 2; Length 592;
Best Local Similarity 69.4%; Pred. No. 1.1e-160;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

QY 1 MALEIHMSPMCLINFNQKVNQAEALISAITQPVVVVAIVGLYRTGKSYLNNKLAG 60
Db 1 MASEIHMTPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLNNKLAG 60
QY 61 KNGKFSVASTVQSHTKGIWCVPHNPNNHTLVLLDTGLGDKVEKADNNDIQLPALAL 120
Db 61 KKGKFSLSGTVQSHTKGIWCVPHNPNNHTLVLLDTGLGDKVEKADNNDIQLPALAV 120
QY 121 LLSSTFVYNTVTKIDQGAIDLHNVNTELTDLKARNSPD--LDRVEDPADSASFFPDVW 178
Db 121 LLSSTFVYNTVTKIDQGAIDLHNVNTELTDLKARNSPD--LDRVEDPADSASFFPDVW 180
QY 179 TLRFCLGLEIDGQVTPDEYLENSLRPKQSDQVQNFNLRCLCIQKFFPKKCFIDL 238
Db 181 TLRFCLGLEIDGQVTPDEYLENSLRPKQSDQVQNFNLRCLCIQKFFPKKCFIDL 240
QY 239 PAHQKLAQLETLPDDELEPEFVQVADFCVYFNSKTKTLGGGIQVNGPRLESILVLT 298
Db 241 PVHRRKLAQLETLPDDELEPEFVQVADFCVYFNSKTKTLGGGIQVNGPRLESILVLT 300
QY 299 VNAISSGDLPCINAVLAQRENSAAVQKAIHAHYDQMGQKQVQLPMTLOELLDLHRTS 358
Db 301 VNAISSGDLPCINAVLAQRENSAAVQKAIHAHYDQMGQKQVQLPMTLOELLDLHRTS 360
QY 359 EREAIEVFMKNSFKVDQSFQKLETLDDAKNDICRKNLEASSDYCSALLKIDFGPLEE 418
Db 361 EREAIEVFMKNSFKVDQSFQKLETLDDAKNDICRKNLEASSDYCSALLKIDFGPLEE 420
QY 419 AVKQGIYKPGGKGNLFIOKTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQ 478
Db 421 EVKAGIYKPGGKGNLFIOKTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQ 480
QY 479 ALTETEKKKKAQVKAABAKAORLAAIQRONEQMOERERLHQEQVQVQVQVQVQVQV 534
Db 481 TLTEKEKEIEVERVKAESAQASAKMLQEMQKQKERSYQEHKQLTKERMENDRV 540
QY 535 NWLAQQ-----KMQEQQ 547
Db 541 QLLKEQERTLALKLOEQE 558

RESULT 5
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US-09-702-705-1809
; Sequence 1809, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1809
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-1809

Query Match      64.4%; Score 1958.5; DB 4; Length 592;
Best Local Similarity 69.4%; Pred. No. 1.le-160;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

QY 1 MALEIHMSPMCLIEFNQKLVNOEALILSAITOPVVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MASEIHMTGPMCLIENTNCRMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKLKAG 60

QY 61 KXKGFSAVSTVQSHTKGIWICVPHPNWPNHTLVLLDTEGLGDEKADKNNDIQIPALAL 120
Db 61 KXKGFSLGSTVQSHTKGIWMCVPHPKPGHILVLVLLDTEGLGDEKADKNNDISWIFALAV 120

QY 121 LLSSTFVYNTVTKIDOGAIDLLHNVTETDLKARNSPD--LDRVEDPADSASFFPDLYW 178
Db 121 LLSSTFVYNSIGTINQAMQDQLYYVTELTNRIRKSSSPDENENEVEDSADFSVFFPDVW 180

QY 179 TLRDFCLGLEIDQVLTPEYLENSLRPKGSDQRVQNFNLPRLCIQKFPFKKCFIFDL 238
Db 181 TLRDFSLDLADQQLTPDEYLYTSLKKGTSQKDETNLPRLCIRKFPFKKCFVDR 240

QY 239 PAHQKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTY 298
Db 241 PVHRRKLAQLEKLQDELDPEFVQVADFCSYIFSNSKTKTLGGGIQVNGPRLESVLTY 300

QY 299 VNAISSGDLPCINAVIALAORENSAAVQKAIHAYDOOMGOKVOLPMETLOELLDLHRTS 358
Db 301 VNAISSGDLPCMENAVIALAQIENSAAVQKAIHAYEQOMGOKVOLPESLQELLDLHRS 360

QY 359 ERAIEVFMKNSFKVDQSFQKELETLLDAKONDICKRNLEASSDYCSALLKDI FGPLEE 418
Db 361 ERAIEVFRSSFKVDVHLFQKELAAQLEKKRDDFCQKQNEASSDRCSGLLQVIFSPLEE 420

QY 419 AVKQGIYSKPGGHNLFTQKTEELKAKYIEPRKGIQAEELVQKYLKSKESVSHAILQTDQ 478
Db 421 EVKAGIYSKPGGYRLFVQKLQDLKKKYYEPRKGIQAEELIQTYLKSKESTDAIQLTDQ 480

QY 479 ALTETETKKKEAQVKAFAEAKAORLAATQORONEQMMQERERLHOQVRO----MEIAKQ 534
Db 481 TLTEKEKEIEVERVKAESAQAASAKMLQEMQKNEQMEQKERSYQEHLLKOLTEKMENDRV 540

QY 535 NWLAEQ-----KMOEQQ 547
Db 541 QLLKEQERTIALKLQEQE 558

RESULT 6
US-09-736-457-1809

US-09-702-705-1809
; Sequence 1809, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1809
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1809

Query Match      64.4%; Score 1958.5; DB 4; Length 592;
Best Local Similarity 69.4%; Pred. No. 1.le-160;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

QY 1 MALEIHMSPMCLIEFNQKLVNOEALILSAITOPVVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MASEIHMTGPMCLIENTNCRMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKLKAG 60

QY 61 KXKGFSAVSTVQSHTKGIWICVPHPNWPNHTLVLLDTEGLGDEKADKNNDIQIPALAL 120
Db 61 KXKGFSLGSTVQSHTKGIWMCVPHPKPGHILVLVLLDTEGLGDEKADKNNDISWIFALAV 120

QY 121 LLSSTFVYNTVTKIDOGAIDLLHNVTETDLKARNSPD--LDRVEDPADSASFFPDLYW 178
Db 121 LLSSTFVYNSIGTINQAMQDQLYYVTELTNRIRKSSSPDENENEVEDSADFSVFFPDVW 180

QY 179 TLRDFCLGLEIDQVLTPEYLENSLRPKGSDQRVQNFNLPRLCIQKFPFKKCFIFDL 238
Db 181 TLRDFSLDLADQQLTPDEYLYTSLKKGTSQKDETNLPRLCIRKFPFKKCFVDR 240

QY 239 PAHQKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTY 298
Db 241 PVHRRKLAQLEKLQDELDPEFVQVADFCSYIFSNSKTKTLGGGIQVNGPRLESVLTY 300

QY 299 VNAISSGDLPCINAVIALAORENSAAVQKAIHAYDOOMGOKVOLPMETLOELLDLHRTS 358
Db 301 VNAISSGDLPCMENAVIALAQIENSAAVQKAIHAYEQOMGOKVOLPESLQELLDLHRS 360

QY 359 ERAIEVFMKNSFKVDQSFQKELETLLDAKONDICKRNLEASSDYCSALLKDI FGPLEE 418
Db 361 ERAIEVFRSSFKVDVHLFQKELAAQLEKKRDDFCQKQNEASSDRCSGLLQVIFSPLEE 420

QY 419 AVKQGIYSKPGGHNLFTQKTEELKAKYIEPRKGIQAEELVQKYLKSKESVSHAILQTDQ 478
Db 421 EVKAGIYSKPGGYRLFVQKLQDLKKKYYEPRKGIQAEELIQTYLKSKESTDAIQLTDQ 480

QY 479 ALTETETKKKEAQVKAFAEAKAORLAATQORONEQMMQERERLHOQVRO----MEIAKQ 534
Db 481 TLTEKEKEIEVERVKAESAQAASAKMLQEMQKNEQMEQKERSYQEHLLKOLTEKMENDRV 540

QY 535 NWLAEQ-----KMOEQQ 547
Db 541 QLLKEQERTIALKLQEQE 558

RESULT 7
US-09-643-657-4
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; Sequence 4, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/09/643,657
; FILING DATE: 17-Aug-2000
; CLASSIFICATION DATA: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 592 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-643-657-4

Query Match 64.4%; Score 1958.5; DB 4; Length 592;
Best Local Similarity 69.4%; Pred. No. 1.le-160;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

Qy 1 MALEIHMSDPMCLIEFNQKVNQAELEILSAITQPVVVAIVGLYRTGSKYLNKLAG 60
Db 1 MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVAIVGLYRTGSKYLNKLAG 60
Qy 61 KKGFSVASTVQSHTKGIWICVPHNPNTLVLLDTTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KKGFSGLSTVQSHTKGIWMCVPHPKPGHILVLLDTTEGLGDVEKADNKNDISWIFALAV 120
Qy 121 LLSSTFVYNTVVKIDQGAIDLHNVTELTDLKARNSPD--LDRVEDPADSASFPFDLVM 178
Db 121 LLSSTFVNSGTINQAMDQIYVTELTTHIRSKSSPDENEVEVSADFSVFPDFVM 180
Qy 179 TLDRFCLEIGDLQVTPDEYLENSLRPKQSDQVQNFNPLRCLCIKFFPKKCFIFDL 238
Db 181 TLDRFSLDEADGQPLTPDEVITYSLKKGTSQKDETFLNPLRCLIRKFFPKKCFVDR 240
Qy 239 PAHQKLAQLETLDPDELEPEFVQVTEFCSYIFSHSWTKLPGGIMVNGSRLKNLVITY 298
Db 241 PVHRKLAQLEKLDPELDPFVQVADFCSYIFSNKTKTLSSGGIYVNGPRLESVLTY 300
Qy 299 VNAISSGDLPCENAVLALAOENSAVQKAIHYDQMGKQVQLPMETLOELDLHRTS 358
Db 301 VNAISSGDLPCMENAVLALAOENSAVQKAIHYEQMGQKQVQLPESLQELDLHRTS 360
Qy 359 EREAIEVFMKNSFKVDQSFQKELETLDDAKNDICKNLEASSDYCSALLKNDIFGPLEE 418
Db 361 EREAIEVIRSFKVDVHLFQKELAAQLEKKRDFCKQNEASSDRCSGLGLQVIFSPLEE 420
Qy 419 AVKGIYSKPGGHNLFIOKTEELKAKYVREPRKGIQAEVLQKYLKSKESVSHAILQTDQ 478
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RESULT 8

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US-09-671-325-1809
; Sequence 1809, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1809
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-671-325-1809
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Query Match 64.4%; Score 1958.5; DB 4; Length 592;
Best Local Similarity 69.4%; Pred. No. 1.le-160;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

Qy 1 MALEIHMSDPMCLIEFNQKVNQAELEILSAITQPVVVAIVGLYRTGSKYLNKLAG 60
Db 1 MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVAIVGLYRTGSKYLNKLAG 60
Qy 61 KKGFSVASTVQSHTKGIWICVPHNPNTLVLLDTTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KKGFSGLSTVQSHTKGIWMCVPHPKPGHILVLLDTTEGLGDVEKADNKNDISWIFALAV 120
Qy 121 LLSSTFVYNTVVKIDQGAIDLHNVTELTDLKARNSPD--LDRVEDPADSASFPFDLVM 178
Db 121 LLSSTFVNSGTINQAMDQIYVTELTTHIRSKSSPDENEVEVSADFSVFPDFVM 180
Qy 179 TLDRFCLEIGDLQVTPDEYLENSLRPKQSDQVQNFNPLRCLCIKFFPKKCFIFDL 238
Db 181 TLDRFSLDEADGQPLTPDEVITYSLKKGTSQKDETFLNPLRCLIRKFFPKKCFVDR 240
Qy 239 PAHQKLAQLETLDPDELEPEFVQVTEFCSYIFSHSWTKLPGGIMVNGSRLKNLVITY 298
Db 241 PVHRKLAQLEKLDPELDPFVQVADFCSYIFSNKTKTLSSGGIYVNGPRLESVLTY 300
Qy 299 VNAISSGDLPCENAVLALAOENSAVQKAIHYDQMGKQVQLPMETLOELDLHRTS 358
Db 301 VNAISSGDLPCMENAVLALAOENSAVQKAIHYEQMGQKQVQLPESLQELDLHRTS 360
Qy 359 EREAIEVFMKNSFKVDQSFQKELETLDDAKNDICKNLEASSDYCSALLKNDIFGPLEE 418
Db 361 EREAIEVIRSFKVDVHLFQKELAAQLEKKRDFCKQNEASSDRCSGLGLQVIFSPLEE 420
Qy 419 AVKGIYSKPGGHNLFIOKTEELKAKYVREPRKGIQAEVLQKYLKSKESVSHAILQTDQ 478
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Db 421 EVKAGIYSGGVYLFVQKLDLKKYBEPKGIQABEILQTLTKSKESMTDAILLQTDQ 480
 QY 479 ALTETKKKKEAQVKAERKAEORLAATQRQNEQMMQERLHQVQRQ----MEIAKQ 534
 Db 481 TLTEKEKEIEVERKAEASQAQAKMLQEMQKNEQMMQEKERSYQSHLKQLTKERMENDRV 540
 QY 535 NWLAEOQ-----KMQEQQ 547
 Db 541 QLLKEQERTLALKLQEQE 558

RESULT 9
 US-08-736-770-5
 ; Sequence 5, Application US/08736770
 ; Patent No. 5871965
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/736,770
 ; FILING DATE: Filed Herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0145 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 591 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 829177
 ; US-08-736-770-5

Query Match 62.3%; Score 1897; DB 2; Length 591;
 Best Local Similarity 63.5%; Pred. No. 2.2e-155;
 Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;
 QY 1 MALEIHMSDDMCLIEFNQKQNEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
 Db 1 MAPEINLPQMSLIDNTKGLVNVPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
 QY 61 KNGKFSVASTVQSHTKGIWICVPHPNWPHNTLVLLDTEGLGDEKADNKNKDIQIFALAL 120
 Db 61 KNGKFSLGSTVSKHTGKIWMVCVPHPKPETHLVLLDTEGLGDIKGDNDNSWIFALAI 120
 QY 121 LLSSTFVYNTVNVKIDQGAIDLLHNVTETLTLKARNSPDLDRVEDPADSASFFPDLVWTL 180
 Db 121 LLSSTFVYNSMGITINQAMQDLHVHTETLTDRIKANSPPGNNSVDDSDADPVSPFPFVWTL 180

QY 181 RDFCLGLIDGOLVTPDEYLENSLRPKGSDORVQNFNLPRLCIOKFFPKKCFIFDLPA 240
 Db 181 RDTLELEVDGPPITADDYLELSLKURGTDKKSKSFNDPRLCIRKFFPKKCFVFDWPA 240
 QY 241 HOKKLAQLETLDPDELEPEFVQVTEFCYSIIFSHSMTKTLPGGIMVNGSRLKNLVLTYN 300
 Db 241 PKYLAHLEQLAKEELNPDFIQVAEFCSYILSHSNVKTLSGGIAVNGPRLSLVLTYN 300
 QY 301 AISSGDLPCINAVIALAQRENSAAVQKAIAYHDOQMGOKVOLPMETLOELDLHRTSER 360
 Db 301 AISSGDLPCMENAVIALAQIENSAAVEKAIAHYEQMGOKVOLPTETLOELDLHRTSER 360
 QY 361 EAEVFMKNSFKVDVDSFOKELETLLDAQNIDCKENLEASDYCSALLKIDFGPLEEAV 420
 Db 361 EAEVFMKNSFKVDVDMFORKIGLAQLEARDDFCKNSKASSDCCMALLQDIFGPLEEDV 420
 QY 421 KGIYSKPGGHNLFQKTEELKAKYVREPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
 Db 421 KGTFSKPGGYRLFQKLELKNKYQVPRKGIQAEVLKYLKSKESVSHAILQTDQAL 480
 QY 481 TETEKKKKEAQVKAERKAEORLAATQRQNEQMMQERLHQVQRQ----MEIAKQNW 536
 Db 481 SEKERAIEVERIKAESAEAAKMLBEIQKKBEMMEQEKESYQEHVKQLTKMERDRAQL 540
 QY 537 LAEQ-----KMQEQQMVFINCFISPLPVTMRVCSGKGEAARSCGSGQGVW 585
 Db 541 MAEQEKTALKLQEQE-----RLKKEGFENESKR---LQKDIW 575

RESULT 10
 US-09-643-657-5
 ; Sequence 5, Application US/09643657
 ; Patent No. 6642024
 ; GENERAL INFORMATION:
 ; APPLICANT: Diane Pennica
 ; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/643,657
 ; FILING DATE: 17-Aug-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/015,089A
 ; FILING DATE: 29-Jan-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hasak, Janet E.
 ; REGISTRATION NUMBER: 28,616
 ; REFERENCE/DOCKET NUMBER: P1056
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1896
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 591 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 ; US-09-643-657-5
 Query Match 62.3%; Score 1897; DB 4; Length 591;

Best Local Similarity 63.5%; Pred. No. 2.2e-155;
Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;
QY 1 MALEIHMSDPNCLNENFNEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
DB 1 MAPEINLPCPMSLIDNTKQGVNFEALKILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
QY 61 KNGFSVASTVQSHTKGIWCVPHNPHTLVLLDTEGLDVEKADKNDIQIFALAL 120
DB 61 KNGFSLGTSVKSHTKGIWCVPHNPHTLVLLDTEGLDVEKADKNDIQIFALAL 120
QY 121 LLSSTFVNTVNTKIDQGAIDLHNVTETLLKARNSPDLRVEDPADSADFFPDLVWL 180
DB 121 LLSSTFVNTVNTKIDQGAIDLHNVTETLLKARNSPDLRVEDPADSADFFPDLVWL 180
QY 181 RDCFLGLEIDQVLPDEYFVNSLPRKQSGDQVQNFNLPRLCICQKPKKCFIDPLA 240
DB 181 RDCFLGLEIDQVLPDEYFVNSLPRKQSGDQVQNFNLPRLCICQKPKKCFIDPLA 240
QY 241 HOKLAQLETLPPDELEPFVQVTEPCSYIFSHSMTKTLPGGIMVNGSRKLNVLTVN 300
DB 241 PKYLAHLEQLKEELNPDFFIEQVAEFCYSYLHSHNVKTLGGIAVNGPRLESVLTVN 300
QY 301 AISSGDLPCENAVLALAQRENSAAVQKAIHAHYDQMGKQVLPMTLOELDLHRTSE 360
DB 301 AISSGDLPCENAVLALAQRENSAAVQKAIHAHYDQMGKQVLPMTLOELDLHRTSE 360
QY 361 EAIEVFMKNSFKVDQSFQKLETLDAKNDICRNLEASSDYCSALLKIDIFGLPEAV 420
DB 361 EAIEVFMKNSFKVDQSFQKLETLDAKNDICRNLEASSDYCSALLKIDIFGLPEAV 420
QY 421 KQGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKESVSHAILQTDQAL 480
DB 421 KQGTFSKPGYRLFTQKLELKNKYQVPRKGIQAEVLKYLKESVSHAILQTDQAL 480
QY 481 TETEKKEAQAQVAEAEKAEQRLAAIQORNEQMGQERLHQBQVRO----MEIAKQW 536
DB 481 SEKEKAIEVERIKAEAEAAKMLBEIQKNEEMMEQKEKSYQEHVKQLTEKMERDRAQ 540
QY 537 LAEQO-----KMOEQMQVFCISPLPVMTRVSCSGEAEARSQSGQGVW 585
DB 541 MAEQEKTALQEQE-----RLKKEGFENESKR---LQKDIW 575

RESULT 11

US-08-736-770-1
; Sequence 1, Application US/08736770
; Patent No. 5871965
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; STREET: Incyte Pharmaceuticals, Inc.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/736,770
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0145 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4186
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 608 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-736-770-1
Query Match 61.8%; Score 1881; DB 2; Length 608;
Best Local Similarity 66.0%; Pred. No. 5.6e-154;
Matches 372; Conservative 78; Mismatches 104; Indels 10; Gaps 3;
QY 1 MALEIHMSDPNCLNENFNEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
DB 1 MALEIHMSDPNCLNENFNEQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
QY 61 KNGFSVASTVQSHTKGIWCVPHNPHTLVLLDTEGLDVEKADKNDIQIFALAL 120
DB 61 KNGFSVASTVQSHTKGIWCVPHNPHTLVLLDTEGLDVEKADKNDIQIFALAL 120
QY 121 LLSSTFVNTVNTKIDQGAIDLHNVTETLLKARNSPDLRVEDPADSADFFPDLVWL 180
DB 121 LLSSTFVNTVNTKIDQGAIDLHNVTETLLKARNSPDLRVEDPADSADFFPDLVWL 180
QY 181 RDCFLGLEIDQVLPDEYFVNSLPRKQSGDQVQNFNLPRLCICQKPKKCFIDPLA 240
DB 181 RDCFLGLEIDQVLPDEYFVNSLPRKQSGDQVQNFNLPRLCICQKPKKCFIDPLA 240
QY 241 HOKLAQLETLPPDELEPFVQVTEPCSYIFSHS-MTKTLPGGIMVNGSRKLNVLTVN 299
DB 241 KXKYLXLEQLKEELNPDFFIEQVAEFCYSYLHSHNVRLFQVALQVNGPRLESVLTVN 300
QY 300 NAISGDLPCENAVLALAQRENSAAVQKAIHAHYDQMGKQVLPMTLOELDLHRTSE 359
DB 300 NAISGDLPCENAVLALAQRENSAAVQKAIHAHYDQMGKQVLPMTLOELDLHRTSE 360
QY 360 REAIEVFMKNSFKVDQSFQKLETLDAKNDICRNLEASSDYCSALLKIDIFGLPEA 419
DB 360 REAIEVFMKNSFKVDQSFQKLETLDAKNDICRNLEASSDYCSALLKIDIFGLPEA 420
QY 420 VKQGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKESVSHAILQTDQA 479
DB 420 VKQGTFSKPGYRLFTQKLELKNKYQVPRKGIQAEVLKYLKESVSHAILQTDQA 480
QY 480 LTETEKKEAQAQVAEAEKAEQRLAAIQORNEQMGQERLHQBQVRO----MEIAKQW 535
DB 480 LSEKEKAIEVERIKAEAEAAKMLBEIQKNEEMMEQKEKSYQEHVKQLTEKMERDRAQ 540
QY 536 WLAEOQ-----KMOEQMQVFCIN 554
DB 541 LMEQEKTLTSKLEQARALKERC 564

RESULT 12

US-09-949-016-8267
; Sequence 8267, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8267
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8267

Query Match 60.2%; Score 1832.5; DB 4; Length 583;
Best Local Similarity 66.2%; Pred. No. 8.2e-150;
Matches 366; Conservative 65; Mismatches 91; Indels 31; Gaps 2;

QY 1 MALEIHMSDPMCLIENTNFNQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 58 MAPEIHMTGPMCLIENTNGLVANPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 117
QY 61 KNGKFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
DB 118 KNGKFSLSGTVSKHTKGIWMCVPHPKPEHTLVLLDTEGLGDVKKGNQNDSWIFTLAV 177
QY 121 LLSSTFVYNTVVKIDOGAIDLLHNVTETDLKARNSPDLDRVEDPADSASFPDDLVTWL 180
DB 178 LLSSTLVYNSMGTINQAMQDQLYVVTETLTHIRSKSPDENENEDSADFVSFPDFVWTL 237
QY 181 RPFCLGLEIDGQLVTPDEYLENSLRPKQSDORVQNFNLPRLCICQKFFPKKCFIFDLPA 240
DB 238 RDFSLEADGQPLTPDEYLEVSLKUTQGTQSKDKNFNLPRLCIRKFFPKKCFVFDLPI 297
QY 241 HOKKLAQLETLPPDELEPEFVQVTEFCYSYIFSHSMTKTLPGGIMVNGSRLKNLVLYYVN 300
DB 298 HRRKLAQLEKLDDELDPEFVQVADFCSYIFSNKTKLSSGIVKNGPRLSLVLYYIN 357
QY 301 AISSGDLPCIENTAVLALAQRENSAAVQKAIADHYDQMGQKQVLPMTTLOELDLHRTSR 360
DB 358 AISRGDLPCMENAVLALAQRENSAAVQKAIADHYDQMGQKQVLPMTTLOELDLHRTSR 415
QY 361 EAIEVPMKNSFKDQVDSQFQKELETLDDAKNDICKNLEASSDYCSALLKDIKDFPLEEAV 420
DB 416 -----LDKRRDDFCQKQNEASSDYCSALLQVIFSPDEEEV 450
QY 421 KQGIYSKPGGHNLFIOKTBELKAKYRPRKGIQAEVQLKYLKSKESVSHAILQTDQAL 480
DB 451 KAGIYSKPGGYCLFIQKLDLEKYYEPRKGIQAEVQLKYLKSKESVSHAILQTDQAL 510
QY 481 TETEKKKKEAQAQVKAEEAKAEQRLAAIQRNEQMQRERLHQEQVRQ-----MEIAKQNW 536
DB 511 TEKEKEIEVCVKAESAQAKMVEBQIKYQOMMEKEKSYQEHVKQLTEKMERERAQL 570
QY 537 LAEQQKMQEQMQ 549
DB 571 LEEQKTLTSKLQ 583

RESULT 13
US-09-643-657-14
; Sequence 14, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
;

; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,657
; FILING DATE: 17-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Haseak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 589 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
; US-09-643-657-14

Query Match 58.0%; Score 1765.5; DB 4; Length 589;
Best Local Similarity 61.7%; Pred. No. 5.2e-144;
Matches 343; Conservative 95; Mismatches 109; Indels 9; Gaps 2;

QY 1 MALEIHMSDPMCLIENTNFNQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MASEIHMSPEMCLIENTEAQLVINOEARILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGKFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
DB 61 KRTGSLGTVQSHTKGIWMCVPHPKKAGQTLVLLDTEGLDEVEKGNQNDICWIFALAV 120
QY 121 LLSSTFVYNTVVKIDOGAIDLLHNVTETDLKARNSPDLDRVEDPADSASFPDDLVTWL 180
DB 121 LLSSTFIYNSIGTINQAMQDQLYVVTETLTLKSKSPDQSDVNSANFVGFPIFVWTL 180
QY 181 RPFCLGLEIDGQLVTPDEYLENSLRPKQSDORVQNFNLPRLCICQKFFPKKCFIFDLPA 240
DB 181 RDFSLEADGQPLTPDEYLETSLALRKGTDETKKFNMPRLCIRKFFPKKCFIFDRPG 240
QY 241 HOKKLAQLETLPPDELEPEFVQVTEFCYSYIFSHSMTKTLPGGIMVNGSRLKNLVLYYVN 300
DB 241 DRKQSLKSWIQEDQKLNKEFVQVAFVTSYIIFSYSGVKTLSGGITVNGPRLKSLVQTYVS 300
QY 301 AISSGDLPCIENTAVLALAQRENSAAVQKAIADHYDQMGQKQVLPMTTLOELDLHRTSR 360
DB 301 AICSGELPCMENAVLTLAQIENSAAVQKAITVYEEQMNKIHMPTETLQELDLHRTSR 360
QY 361 EAIEVPMKNSFKDQVDSQFQKELETLDDAKNDICKNLEASSDYCSALLKDIKDFPLEEAV 420
DB 361 EAIEVPMKNSFKDQVDSQFQKELEGAQLEAKRDAFVKKNMDMSSAHCSDLLLEGLFAHLEEEV 420
QY 421 KQGIYSKPGGHNLFIOKTBELKAKYRPRKGIQAEVQLKYLKSKESVSHAILQTDQAL 480
DB 421 KQGTFFKPGGYLFLQKQKEKKYLOTEGKGLQAEVMLRKFKESKEDLADTLKNDQSL 480
QY 481 TETEKKKKEAQAQVKAEEAKAEQRLAAIQRNEQMQRERLHQEQVRQ-----MEIAKQNW 536
DB 481 TEKEKEIEVKAEEAANRALAEMQKHEMLMEQKESQYQEHMKQLTEKMEQERKEL 540
QY 537 LAEQQ-----KMQEQQ 547
DB 541 MAEQQRILSLKQEQE 556


```
RESULT 14
US-09-643-657-15
; Sequence 15, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,657
; FILING DATE: 17-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-643-657-15
Query Match 57.8%; Score 1459.5; DB 4; Length 591;
Best Local Similarity 63.3%; Pred. No. 2.6e-143;
Matches 346; Conservative 82; Mismatches 116; Indels 3; Gaps 1;
Qy 1 MALETHMSDPMLCTIENFNEQLKVNQEALEILSAITOPVVAIVGLYRTGKSYLMNKLKAG 60
Db 3 MASEHMLQPMCLTENTBAHLVINQEALEILSAINQPVVAIVGLYRTGKSYLMNKLKAG 62
Qy 61 KNGKFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTGEGLDGVEKADKNKDIOIFALAL 120
Db 63 KRTGSLGSTVQSHTKGIWICVPHPKAGQTLVLLDTGEGLDGVEKQNDQNDWIFALAV 122
Qy 121 LLSSTFVYNTVKNIDQGAIDLHNVTETDLLKARNSPDLDRVEDPADSASFFPDVLTWL 180
Db 123 LLSSTFVYNSMGNTINQQAQMDQLHYVTELTDLIKSSPDQSGIDDSANFVGFPTFWAL 182
Qy 181 RDFCLGLIDQLVTPDPDYLENLSPKGSQORVONFNLPLCTOKPFPKCKCIFDLP 240
Db 183 RDFSLELVNGKLVTPDPDYLEHSLTLKKGADKTKTFSEPRLCIRKFPKPKCIFDRPA 242
Qy 241 HOKLAQLETLPPDDLEPEFVQVTEFCYSIFSHMTKTLPGGMVNGSRKLNKLVLTYN 300
Db 243 LRKQCKLETLGEEELCESEFVEQVAETSYIFSAVTKLGGIIVNGPRKLSVQTYVG 302
Qy 301 AISSGDLPCIEAVLALAQRENSAAVQKAIAYHQDMQKQVQLPMETIQEILLDLHRTSR 360
Db 303 AISSGSLFCMESAVLTLAQIENSAVQKAIYHBEQMNQKIQMPETIQEILLDLHRLIER 362
Qy 361 EAIEVFMQNSPKVDQSKFQKLETLDDAKQNDICRNLKLEASDYCSALLKDIQFPLEAV 420
Db 361 EAIEVFMQNSPKVDQSKFQKLETLDDAKQNDICRNLKLEASDYCSALLKDIQFPLEAV 420
Db 363 EAIEVFMQNSPKVDQSKFQKLETLDDAKQNDICRNLKLEASDYCSALLKDIQFPLEAV 422
Qy 421 KQGIYSKPGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Db 423 KQGTFSKPGGYFLFQMEQLEKKYQAPKGLAEAVLKKYFESKEDIVETLLKTDQSL 482
Qy 481 TETEKKKKEAQVKAFAEAKAEQRLAAIQORNEQMMQERLHQEVRQMEIAKQNWLABQ 540
Db 483 TEAAKEIEVERIKABTAANRELAERAEKQKFTELMMQKEESYQEHVRQL---TERMKESQ 539
Qy 541 QKMOEQQ 547
Db 540 KKLIEEQ 546
RESULT 15
US-09-643-657-13
; Sequence 13, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,657
; FILING DATE: 17-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-643-657-13
Query Match 48.0%; Score 1459.5; DB 4; Length 620;
Best Local Similarity 51.2%; Pred. No. 1.6e-117;
Matches 281; Conservative 118; Mismatches 145; Indels 5; Gaps 2;
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Db 1 MEAPICLVENWKNQLTVNLEAIRILEQIAQLVVAIVGLYRTGKSYLMNKLKAGNKHGS 60
Qy 67 VASTVQSHTKGIWICVPHPNPNHTLVLLDTGEGLDGVEKADKNKDIOIFALALLSSTF 126
Db 61 LGSTVQSETKGIWICVPHPKPTKPTHTLVLLDTGEGLDGVEKQNDQNDWIFALAVLLSSTF 120
Qy 127 VYNTVKNIDQGAIDLHNVTETDLLKARNSPDLDRVEDPADSASFFPDVLTWLDRDCLG 186
Db 121 VYNSMSTINQQAQLHQLFVTELTQLIRAKSPREDKVKDSSEFVGFPPDFIWAVERDALE 180
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 20, 2005, 13:29:02 ; Search time 136 Seconds
(without alignments)
1453.632 Million cell updates/sec

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Perfect score: 3043
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

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14: /cgn2_6/ptodata1/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata1/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata1/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata1/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata1/1/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query #		DB	ID	Description
		Match	Length			
1	2815	92.5	586	14	US-10-028-072-46	Sequence 46, Appl
2	2815	92.5	586	14	US-10-140-808-46	Sequence 46, Appl
3	2815	92.5	586	14	US-10-121-049-46	Sequence 46, Appl
4	2815	92.5	586	14	US-10-123-904-46	Sequence 46, Appl
5	2815	92.5	586	14	US-10-140-470-46	Sequence 46, Appl
6	2815	92.5	586	14	US-10-175-746-46	Sequence 46, Appl
7	2815	92.5	586	14	US-10-176-918-46	Sequence 46, Appl
8	2815	92.5	586	14	US-10-176-921-46	Sequence 46, Appl
9	2815	92.5	586	14	US-10-137-865-46	Sequence 46, Appl
10	2815	92.5	586	14	US-10-140-474-46	Sequence 46, Appl
11	2815	92.5	586	14	US-10-142-431-46	Sequence 46, Appl
12	2815	92.5	586	14	US-10-143-114-46	Sequence 46, Appl
13	2815	92.5	586	14	US-10-142-419-46	Sequence 46, Appl

ALIGNMENTS

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RESULT 1
US-10-028-072-46
; Sequence 46, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Berge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flinnvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/000000
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17

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; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match      92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLINFEQKVNQAELEILSAITQPVVVAIVGLYRTGKSYLWKLKAG 60
Db 1 MALEIHMSDPMCLINFEQKVNQAELEILSAITQPVVVAIVGLYRTGKSYLWKLKAG 60

Qy 61 KNGFSVASTVQSHTKGIWCVPHNPWNTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KNGFSVASTVQSHTKGIWCVPHNPWNTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLRVEDPADSASFFPDVWTL 180

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Qy 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN 300
Db 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN 300

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Db 301 AISSGDLPCIEENAVLALAORENSAAVQKAIHYDQMGOKVQLPMTLQELLDLHRTSER 360

Qy 361 EAI EVFMKNSPKVDQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Db 361 EAI EVFMKNSPKVDQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420

Qy 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQKYLKSKESVSHAILQTDQAL 480

Qy 481 TETEKKKAEQVKAEEKAEKAEQRLAAIORQNEQMMQERERLHQEVQVROMETAKQNWLAEQ 540
Db 481 TETEKKKAEQVKAEEKAEKAEQRLAAIORQNEQMMQERERLHQEVQVROMETAKQNWLAEQ 540

Qy 541 QKMQEQQM 549
Db 541 QKMQEQQM 549
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RESULT 2

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US-10-140-808-46
; Sequence 46, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

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; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Sherwood, Steven
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; PRIORITY FILING DATE: 2002-05-07
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-46
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Query Match      92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 KNGFSVASTVQSHTKGIWCVPHNPWNTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KNGFSVASTVQSHTKGIWCVPHNPWNTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLRVEDPADSASFFPDVWTL 180

Qy 181 RDFCLGLEIDQVLTDPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPKCKCFIDPLA 240
Db 181 RDFCLGLEIDQVLTDPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPKCKCFIDPLA 240

Qy 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN 300
Db 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLYVN 300

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Db 301 AISSGDLPCIEENAVLALAORENSAAVQKAIHYDQMGOKVQLPMTLQELLDLHRTSER 360

Qy 361 EAI EVFMKNSPKVDQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Db 361 EAI EVFMKNSPKVDQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420

Qy 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQKYLKSKESVSHAILQTDQAL 480

Qy 481 TETEKKKAEQVKAEEKAEKAEQRLAAIORQNEQMMQERERLHQEVQVROMETAKQNWLAEQ 540
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RESULT 3
US-10-121-049-46
; Sequence 46, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MALEIHMSDPMCLIEFNQKLVNQEALBILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
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DB 61 KNGGFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTTEGLDGVKADKNNDIQIFALAL 120
QY 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDCLKARNSPDLDRVEDPADSASFPDVLVWTL 180
DB 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDCLKARNSPDLDRVEDPADSASFPDVLVWTL 180
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DB 241 HQKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVITYYN 300
QY 301 A1SSGDLPC1ENAVLALAORENSAAVQKAIHYDQMGQKQVLPMTTLOELLDLHRTSER 360
DB 301 A1SSGDLPC1ENAVLALAORENSAAVQKAIHYDQMGQKQVLPMTTLOELLDLHRTSER 360
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; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSDPMCLIEFNQKLVNQEALBILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALEIHMSDPMCLIEFNQKLVNQEALBILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGGFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTTEGLDGVKADKNNDIQIFALAL 120
DB 61 KNGGFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTTEGLDGVKADKNNDIQIFALAL 120
QY 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDCLKARNSPDLDRVEDPADSASFPDVLVWTL 180
DB 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDCLKARNSPDLDRVEDPADSASFPDVLVWTL 180
QY 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
QY 241 HQKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVITYYN 300
DB 241 HQKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVITYYN 300
QY 301 A1SSGDLPC1ENAVLALAORENSAAVQKAIHYDQMGQKQVLPMTTLOELLDLHRTSER 360
DB 301 A1SSGDLPC1ENAVLALAORENSAAVQKAIHYDQMGQKQVLPMTTLOELLDLHRTSER 360
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DB 361 EAIEVFMKNSFKVDQGSFQKELETLDDAKNDICRKNLEASSDYCSALLKIDIFGPLEEAV 420
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QY 421 KQIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 421 KQIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
QY 481 TETEKKKKAEQVKAEEAKAEQRLAAIORQNEQMMQERERLHOEVRQMEIAKQNWLAQ 540
DB 481 TETEKKKKAEQVKAEEAKAEQRLAAIORQNEQMMQERERLHOEVRQMEIAKQNWLAQ 540
QY 541 QKMQEQQMQ 549
DB 541 QKMQEQQMQ 549
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C150
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEIHMSDPCLNIENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALEIHMSDPCLNIENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTGEGLDVEKADKNDIQIFALAL 120
DB 61 KNGGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTGEGLDVEKADKNDIQIFALAL 120
QY 121 LLSSTFFVNTVNTKIDQGAIDLLHNVTETDLKARNSPDLDRVEDPADSASFFPDVWTL 180
DB 121 LLSSTFFVNTVNTKIDQGAIDLLHNVTETDLKARNSPDLDRVEDPADSASFFPDVWTL 180
QY 181 RDCFLGLEIDQGLVTPDPEYLENSLRPKQSGDQORVQNFNLPRLCIQKFFPKKCFIDLPA 240
DB 181 RDCFLGLEIDQGLVTPDPEYLENSLRPKQSGDQORVQNFNLPRLCIQKFFPKKCFIDLPA 240
QY 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTVYN 300
DB 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTVYN 300

QY 301 AISSGDLPCIEENAVLALAQRENSAAVQKAIHAYDOOMQGVOLPMETLOELLDLHRTSER 360
DB 301 AISSGDLPCIEENAVLALAQRENSAAVQKAIHAYDOOMQGVOLPMETLOELLDLHRTSER 360
QY 361 EAEIVFMKNSFKVDVDSFQKELETLLDAKNDICRNLKASDYCSALLKDIIFGPLEEAV 420
DB 361 EAEIVFMKNSFKVDVDSFQKELETLLDAKNDICRNLKASDYCSALLKDIIFGPLEEAV 420
QY 421 KQIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 421 KQIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
QY 481 TETEKKKKAEQVKAEEAKAEQRLAAIORQNEQMMQERERLHOEVRQMEIAKQNWLAQ 540
DB 481 TETEKKKKAEQVKAEEAKAEQRLAAIORQNEQMMQERERLHOEVRQMEIAKQNWLAQ 540
QY 541 QKMQEQQMQ 549
DB 541 QKMQEQQMQ 549
RESULT 6
US-10-175-746-46
; Sequence 46, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEIHMSDPCLNIENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALEIHMSDPCLNIENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTGEGLDVEKADKNDIQIFALAL 120
DB 61 KNGGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTGEGLDVEKADKNDIQIFALAL 120
QY 121 LLSSTFFVNTVNTKIDQGAIDLLHNVTETDLKARNSPDLDRVEDPADSASFFPDVWTL 180
DB 121 LLSSTFFVNTVNTKIDQGAIDLLHNVTETDLKARNSPDLDRVEDPADSASFFPDVWTL 180
QY 181 RDCFLGLEIDQGLVTPDPEYLENSLRPKQSGDQORVQNFNLPRLCIQKFFPKKCFIDLPA 240

181	Db	ROFCLEIGDGLVTPDEYLENSLRPKQGSQDORVQNFNLRCLCIQFFPKKCFIDPLPA	240
241	Qy	HQKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRKLNVLTYYN	300
241	Db	HQKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRKLNVLTYYN	300
301	Qy	ATSSGDLPCIEANVALAORENSAAVOKAIAHYDQMGQKVQLPMETLQELLDLHETSR	360
301	Db	ATSSGDLPCIEANVALAORENSAAVOKAIAHYDQMGQKVQLPMETLQELLDLHETSR	360
361	Qy	EATIEVFMKNSFKDVQDSFQKELETLDDAKONDI CKRNLEASSDYCSALLKDI FGPLEEAV	420
361	Db	EATIEVFMKNSFKDVQDSFQKELETLDDAKONDI CKRNLEASSDYCSALLKDI FGPLEEAV	420
421	Qy	KQGIYSKPGGHNLFIQKTEELKAKYRPRXIGIOAEVLOKYLKSKESVSHALQTDDAL	480
421	Db	KQGIYSKPGGHNLFIQKTEELKAKYRPRXIGIOAEVLOKYLKSKESVSHALQTDDAL	480
481	Qy	TETEKKKKEAQVKAEEAKAEQAORLAAIORQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ	540
481	Db	TETEKKKKEAQVKAEEAKAEQAORLAAIORQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ	540
541	Qy	QKMQEQQM 549	
541	Db	QKMQEQQM 549	

RESULT 7
IIS-10-176-918-46

US-10-176-918-46
; Sequence 46, Application US/10176918
; Publication No. US20030027275A1

; GENERAL INFORMATION:

APPLICANT:	Baker, Kevin P.
APPLICANT:	Beresini, Maureen
APPLICANT:	DeForge, Laura
APPLICANT:	Desnoyers, Luc
APPLICANT:	Filvaroff, Ellen
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowsky, Paul J.
APPLICANT:	Gurney, Austin L.
APPLICANT:	Sherwood, Steven
APPLICANT:	Smith, Victoria
APPLICANT:	Stewart, Timothy A
APPLICANT:	Tumas, Daniel
APPLICANT:	Watanabe, Colin K
APPLICANT:	Wood, William
APPLICANT:	Zhang, Zemin

; AFFILIATION: ZIGANG, ZEMIAN
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C382

; CURRENT APPLICATION NUMBER: US/10/176,918
 ; CURRENT FILING DATE: 2002-06-20

;
;
Prior App:

; NUMBER OF

; SEQ ID NO 46

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; LENGTH: 586

```

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy		1	MALETHMSDPMCLIEFNENQLKVNQBALEIILSAITQPWWVAIVGLVTRTGKSYLMNKL	60
pB		1	MALETHMSDPMCLIEFNENQLKVNQBALEIILSAITQPWWVAIVGLVTRTGKSYLMNKL	60

Qy 61 KNKGFSVASTVQSHTKGIWTCVPHNPWPHNTLVLLDTEGLGDVEKADKNNDIQIFALAL 120

Db	61	KNKGFSAVSTVQSHTKGIWICVPHPNWPNHTVLVLLDTEGLGDVEKADKNQNDIQIFALAL	120
Qy	121	LLSSTFVYNTVNTKIDQGAIDLHNVTETDLLKARNSPDLDRVEDPADSAPFPDLVWTL	180
Db	121	LLSSTFVYNTVNTKIDQGAIDLHNVTETDLLKARNSPDLDRVEDPADSAPFPDLVWTL	180
Qy	181	RDFCIGLEIDQGLVTPDDYLENSLRPKGSDQRQVQNFNLPRLCIOKFPKKKCFIFDLP	240
Db	181	RDFCIGLEIDQGLVTPDDYLENSLRPKGSDQRQVQNFNLPRLCIOKFPKKKCFIFDLP	240
Qy	241	HOKKLAQLETLTPDDELEPEFVQVTFECYSIFPSHMTKTLPGGIMVNGSRLLKNLVLYVN	300
Db	241	HOKKLAQLETLTPDDELEPEFVQVTFECYSIFPSHMTKTLPGGIMVNGSRLLKNLVLYVN	300
Qy	301	AISSGDLPCINAVLALAQRENSAAVQKAIHAHYDQMGQKVQLPMETLOQLDLHRTSR	360
Db	301	AISSGDLPCINAVLALAQRENSAAVQKAIHAHYDQMGQKVQLPMETLOQLDLHRTSR	360
Qy	361	EAEIVFMKNSFKVDQSFQKELETLTLLDKQNDIKRNLEASDYSALLKIDIFGPLEEAV	420
Db	361	EAEIVFMKNSFKVDQSFQKELETLTLLDKQNDIKRNLEASDYSALLKIDIFGPLEEAV	420
Qy	421	KQGIYKPGGHNLFQKXTEELKAKYRYRBRKIGIQAEVLQKYLKSKESVSHAILQTDQAL	480
Db	421	KQGIYKPGGHNLFQKXTEELKAKYRYRBRKIGIQAEVLQKYLKSKESVSHAILQTDQAL	480
Qy	481	TETEKKKKEAQVKAEAEKAEQRLAAIQRONEQMMQERERLHQEVROMEIAKQNWLAEQ	540
Db	481	TETEKKKKEAQVKAEAEKAEQRLAAIQRONEQMMQERERLHQEVROMEIAKQNWLAEQ	540
Qy	541	QKMQSQMQQ 549	
Db	541	QKMQSQMQQ 549	

RESULT 8

US-10-176-921-46

; Sequence 46, Application US/10176921

; Publication No. US20030027276A1

: GENERAL INFORMATION:

APPLICANT:	Baker, Kevin P.
APPLICANT:	Beresini, Maureen
APPLICANT:	DeForge, Laura
APPLICANT:	Desnoyers, Luc
APPLICANT:	Filvaroff, Ellen
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Gurney, Austin L.
APPLICANT:	Sherwood, Steven
APPLICANT:	Smith, Victoria
APPLICANT:	Stewart, Timothy A
APPLICANT:	Tamas, Daniel
APPLICANT:	Watanabe, Colin K
APPLICANT:	Wood, William
APPLICANT:	Zhang, Zemin

APPLICANT: Zing, Zemi
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C288

; CURRENT APPLICATION NUMBER: US/10/176,921

;
;
CURRENT FILE

Prior Application

NUMBER OF SE

; SEQ ID NO 4

; LENGTH: 586

```

; TYPE: PRT

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Query Match	92.5%;	Score 2815;	DB 14;	Length 586;
Best Local Similarity	100.0%;	Pred. No. 8.2e-197;		
Matches 549:	Conservative	0;	Mismatches 0;	Indels 0


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; FILE REFERENCE: P3330RIC162
; CURRENT APPLICATION NUMBER: US/10/140,474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-474-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSPMCLINFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MALEIHMSPMCLINFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
QY 61 KKGFSVASTVQSHTKGIWICVPHPNPNHNTLVLLDTGLGDEVKADNKNDIQIFALAL 120
Db 61 KKGFSVASTVQSHTKGIWICVPHPNPNHNTLVLLDTGLGDEVKADNKNDIQIFALAL 120
QY 121 LLSSTFVYNTVTKIDQGAIDLHNVTETDLLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVTKIDQGAIDLHNVTETDLLKARNSPDLDRVEDPADSASFFPDVWTL 180
QY 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFPFKKCFIPDLPA 240
Db 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFPFKKCFIPDLPA 240
QY 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRLKNLVITYN 300
Db 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRLKNLVITYN 300
QY 301 ATSSGDLPCIEANVALAORENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSER 360
Db 301 ATSSGDLPCIEANVALAORENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSER 360
QY 361 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICRKNLEASDDYCSALLKDI FGPLEEAV 420
Db 361 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICRKNLEASDDYCSALLKDI FGPLEEAV 420
QY 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
QY 481 TETEKKKKEAQAQKAEAEKAEQAORLAAIQRNEQMMQERERLHQBQVROMEIAKQNWLAEQ 540
Db 481 TETEKKKKEAQAQKAEAEKAEQAORLAAIQRNEQMMQERERLHQBQVROMEIAKQNWLAEQ 540
QY 541 QKMQEQQM 549
Db 541 QKMQEQQM 549

RESULT 11
US-10-142-431-46
; Sequence 46, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
```

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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-03-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-431-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSPMCLINFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MALEIHMSPMCLINFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
QY 61 KKGFSVASTVQSHTKGIWICVPHPNPNHNTLVLLDTGLGDEVKADNKNDIQIFALAL 120
Db 61 KKGFSVASTVQSHTKGIWICVPHPNPNHNTLVLLDTGLGDEVKADNKNDIQIFALAL 120
QY 121 LLSSTFVYNTVTKIDQGAIDLHNVTETDLLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVTKIDQGAIDLHNVTETDLLKARNSPDLDRVEDPADSASFFPDVWTL 180
QY 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFPFKKCFIPDLPA 240
Db 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFPFKKCFIPDLPA 240
QY 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRLKNLVITYN 300
Db 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRLKNLVITYN 300
QY 301 ATSSGDLPCIEANVALAORENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSER 360
Db 301 ATSSGDLPCIEANVALAORENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSER 360
QY 361 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICRKNLEASDDYCSALLKDI FGPLEEAV 420
Db 361 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICRKNLEASDDYCSALLKDI FGPLEEAV 420
QY 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
QY 481 TETEKKKKEAQAQKAEAEKAEQAORLAAIQRNEQMMQERERLHQBQVROMEIAKQNWLAEQ 540
Db 481 TETEKKKKEAQAQKAEAEKAEQAORLAAIQRNEQMMQERERLHQBQVROMEIAKQNWLAEQ 540
QY 541 QKMQEQQM 549
Db 541 QKMQEQQM 549

RESULT 12
US-10-143-114-46
; Sequence 46, Application US/10143114
; Publication No. US20030036180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
```

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; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-114-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSDPMCLIEFNFEQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
DB 1 MALEIHMSDPMCLIEFNFEQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60

QY 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTGEGLDVKEADKNNDIQIFALAL 120
DB 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTGEGLDVKEADKNNDIQIFALAL 120

QY 121 LLSSTFVNTVNTKIDQGAIDLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVLTWL 180
DB 121 LLSSTFVNTVNTKIDQGAIDLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVLTWL 180

QY 181 RDFCLGLEIDQGLVTPDDEYLENSLRPKQGSQDQVQNFNLPRLCIQKFFPKKCFIDPLA 240
DB 181 RDFCLGLEIDQGLVTPDDEYLENSLRPKQGSQDQVQNFNLPRLCIQKFFPKKCFIDPLA 240

QY 241 HQKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGIIMVNGSRKLNVLITYVN 300
DB 241 HQKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGIIMVNGSRKLNVLITYVN 300

QY 301 AISSGDLPCIEENAVLALAQRNSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360
DB 301 AISSGDLPCIEENAVLALAQRNSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360

QY 361 EAI EFMKNSFKVDQSFQKELETLLDAKQNDICRNL EASSDYCSALLKDI FGPLEEAV 420
DB 361 EAI EFMKNSFKVDQSFQKELETLLDAKQNDICRNL EASSDYCSALLKDI FGPLEEAV 420

QY 421 KOGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
DB 421 KOGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480

QY 481 TETEKKKKEAQVKA EAKAEAKAORLAAIQRQNEQMQERLHQEVQVQMEIAKQNWLAEQ 540
DB 481 TETEKKKKEAQVKA EAKAEAKAORLAAIQRQNEQMQERLHQEVQVQMEIAKQNWLAEQ 540

QY 541 QKMQEQMQ 549
DB 541 QKMQEQMQ 549

RESULT 13
US-10-142-419-46
; Sequence 46, Application US/10142419
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; Publication No. US2003004945A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C244
; CURRENT APPLICATION NUMBER: US/10/142,419
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-419-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSDPMCLIEFNFEQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
DB 1 MALEIHMSDPMCLIEFNFEQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60

QY 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTGEGLDVKEADKNNDIQIFALAL 120
DB 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTGEGLDVKEADKNNDIQIFALAL 120

QY 121 LLSSTFVNTVNTKIDQGAIDLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVLTWL 180
DB 121 LLSSTFVNTVNTKIDQGAIDLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVLTWL 180

QY 181 RDFCLGLEIDQGLVTPDDEYLENSLRPKQGSQDQVQNFNLPRLCIQKFFPKKCFIDPLA 240
DB 181 RDFCLGLEIDQGLVTPDDEYLENSLRPKQGSQDQVQNFNLPRLCIQKFFPKKCFIDPLA 240

QY 241 HQKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGIIMVNGSRKLNVLITYVN 300
DB 241 HQKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGIIMVNGSRKLNVLITYVN 300

QY 301 AISSGDLPCIEENAVLALAQRNSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360
DB 301 AISSGDLPCIEENAVLALAQRNSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360

QY 361 EAI EFMKNSFKVDQSFQKELETLLDAKQNDICRNL EASSDYCSALLKDI FGPLEEAV 420
DB 361 EAI EFMKNSFKVDQSFQKELETLLDAKQNDICRNL EASSDYCSALLKDI FGPLEEAV 420

QY 421 KOGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
DB 421 KOGIYKPGGHNLFQKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480

QY 481 TETEKKKKEAQVKA EAKAEAKAORLAAIQRQNEQMQERLHQEVQVQMEIAKQNWLAEQ 540
DB 481 TETEKKKKEAQVKA EAKAEAKAORLAAIQRQNEQMQERLHQEVQVQMEIAKQNWLAEQ 540

QY 541 QKMQEQMQ 549
```

```
Db          541 QKMQEQQM 549
|||||
RESULT 14
US-10-123-262-46
; Sequence 46, Application US/10123262
; Publication No. US20030049816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC38
; CURRENT APPLICATION NUMBER: US/10/123,262
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-262-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MALEIHMSDPMCLIEFNENQKVNQEALEILSAITOPVVVVAIVGLYRTGKSYLMNKL 60
Db      1 MALEIHMSDPMCLIEFNENQKVNQEALEILSAITOPVVVVAIVGLYRTGKSYLMNKL 60

QY      61 KNGGFSVASTVQSHTKGIWICVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFAL 120
Db      61 KNGGFSVASTVQSHTKGIWICVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFAL 120

QY      121 LLSSTFVYNTVANKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVT 180
Db      121 LLSSTFVYNTVANKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVT 180

QY      181 RDFCLGLEIDGQVLTPEDELEPEFVQVTFECSYIFSHSMTKTLPGGIWNGSRLKNLVLYTN 240
Db      181 RDFCLGLEIDGQVLTPEDELEPEFVQVTFECSYIFSHSMTKTLPGGIWNGSRLKNLVLYTN 240

QY      241 HQKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIWNGSRLKNLVLYTN 300
Db      241 HQKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIWNGSRLKNLVLYTN 300

QY      301 AISSGDLPCIEANAVLALAQRENSAAVQKAIHYDQMGQKQVLPMTTQELLDLHRTSER 360
Db      301 AISSGDLPCIEANAVLALAQRENSAAVQKAIHYDQMGQKQVLPMTTQELLDLHRTSER 360

QY      361 EALEVFMKNSFKDQDSFOKELETLDAKQNDICKENLEASSDYCSALLKDIIPGLEEAV 420
Db      361 EALEVFMKNSFKDQDSFOKELETLDAKQNDICKENLEASSDYCSALLKDIIPGLEEAV 420

QY      421 KQGIYKPGGHNLFIQKTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQAL 480
|||||
Db          541 QKMQEQQM 549
|||||
RESULT 15
US-10-142-423-46
; Sequence 46, Application US/10142423
; Publication No. US20030049817A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC249
; CURRENT APPLICATION NUMBER: US/10/142,423
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-423-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MALEIHMSDPMCLIEFNENQKVNQEALEILSAITOPVVVVAIVGLYRTGKSYLMNKL 60
Db      1 MALEIHMSDPMCLIEFNENQKVNQEALEILSAITOPVVVVAIVGLYRTGKSYLMNKL 60

QY      61 KNGGFSVASTVQSHTKGIWICVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFAL 120
Db      61 KNGGFSVASTVQSHTKGIWICVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFAL 120

QY      121 LLSSTFVYNTVANKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVT 180
Db      121 LLSSTFVYNTVANKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVT 180

QY      181 RDFCLGLEIDGQVLTPEDELEPEFVQVTFECSYIFSHSMTKTLPGGIWNGSRLKNLVLYTN 240
Db      181 RDFCLGLEIDGQVLTPEDELEPEFVQVTFECSYIFSHSMTKTLPGGIWNGSRLKNLVLYTN 240

QY      241 HQKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIWNGSRLKNLVLYTN 300
Db      241 HQKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIWNGSRLKNLVLYTN 300

QY      301 AISSGDLPCIEANAVLALAQRENSAAVQKAIHYDQMGQKQVLPMTTQELLDLHRTSER 360
Db      301 AISSGDLPCIEANAVLALAQRENSAAVQKAIHYDQMGQKQVLPMTTQELLDLHRTSER 360
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```

Qy 361 EAIEVFMKNSFKVDVDSFOKELETLLDAKONDICKRNLEASSDYCSALLKDI FGPLEEAV 420
Db 361 EAIEVFMKNSFKVDVDSFOKELETLLDAKONDICKRNLEASSDYCSALLKDI FGPLEEAV 420
Qy 421 KGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVLOKYLKSKSVSHAILQTDQAL 480
Db 421 KGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVLOKYLKSKSVSHAILQTDQAL 480
Qy 481 TETEKKKKEAQVKAEEAKAEQRLAAIQONEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
Db 481 TETEKKKKEAQVKAEEAKAEQRLAAIQONEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
Qy 541 QKMQEQQMQ 549
Db 541 QKMQEQQMQ 549

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Search completed: May 20, 2005, 13:44:05
 Job time : 138 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 20, 2005, 13:09:27 ; Search time 42 Seconds
(without alignments)
1353.907 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHMSDPMCLIFNEQ.....GEARSCGQGVMSQKVVW 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1958.5	64.4	592	2 A41268	guanine nucleotide
2	1897	62.3	591	2 S70524	guanine nucleotide
3	1765.5	58.0	589	2 A46459	macrophage-activat
4	1757.5	57.8	591	2 S43506	hypothetical prote
5	1365.5	44.9	623	2 I49684	guanylate binding
6	251.5	8.3	555	2 T17320	hypothetical prote
7	216	7.1	217	2 A84810	probable guanylate
8	213.5	7.0	991	2 H86188	hypothetical prote
9	171.5	5.6	4574	2 G02520	plectin - human
10	171.5	5.6	4684	2 A59404	plectin (imported)
11	160.5	5.3	1291	2 T22382	hypothetical prote
12	160.5	5.3	1690	2 T13030	microtubule bindin
13	160.5	5.3	4687	1 A39638	plectin - rat
14	159.5	5.2	862	2 T49593	hypothetical prote
15	158	5.2	464	2 H90279	microtubule bindin
16	156.5	5.1	1410	1 A57013	early endosome ant
17	155.5	5.1	762	2 T50155	hypothetical prote
18	154.5	5.1	853	2 T23697	hypothetical prote
19	154.5	5.1	1392	2 A43356	microtubule-vesicl
20	154.5	5.1	1427	2 S22695	restin - human
21	153	5.0	944	2 S26710	spindle pole body
22	151.5	5.0	992	2 T46337	hypothetical prote
23	151	5.0	1290	2 A55094	chromosomal protei
24	151	5.0	1818	1 S73852	hypothetical prote
25	148	4.9	577	1 S39804	moesin - pig
26	148	4.9	1288	2 T46486	chromosomal protei
27	147.5	4.8	429	2 S29565	apolipoprotein A-I
28	147.5	4.8	1790	2 S67593	transport protein
29	147	4.8	407	2 S23325	M2 protein precurs

30	146	4.8	586	1 B41129	ezrin - mouse
31	146	4.8	742	2 S56337	hypothetical prote
32	146	4.8	925	2 T01384	hypothetical prote
33	145.5	4.8	1426	2 T00337	hypothetical prote
34	145	4.8	742	2 C91265	probable vimentin
35	145	4.8	742	2 H86105	probable vimentin
36	145	4.8	1178	2 S78475	mannosylphosphoryl
37	144	4.7	871	2 D86355	protein T16E15.12
38	144	4.7	980	2 E71606	hypothetical prote
39	143.5	4.7	864	2 B90395	purine NTPase [imp
40	143.5	4.7	1875	2 S38173	myosin-like protei
41	143.5	4.7	1992	2 A47297	myosin heavy chain
42	142.5	4.7	1164	2 T24806	hypothetical prote
43	142.5	4.7	2442	2 T08621	centrosome associa
44	142	4.7	657	2 S05517	lamin - chicken
45	142	4.7	1972	1 A41604	myosin heavy chain

ALIGNMENTS

RESULT 1

A41268

guanine nucleotide-binding protein 1 - human

C:Species: Homo sapiens (man)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C:Accession: A41268

R:Cheng, Y.S.E.; Patterson, C.E.; Staeheli, P.

Mol. Cell. Biol. 11, 4717-4725, 1991

A:Title: Interferon-induced guanylate-binding proteins lack an N(T)KXD consensus motif a

A:Reference number: A41268; MUID:91342675; PMID:1715024

A:Accession: A41268

A:Molecule type: mRNA

A:Residues: 1-592 <CHE>

A:Cross-references: UNIPROT:P32455; GB:M55542; NID:g183001; PIDN:AAA35871.1; PID:g183002

C:Genetics:

A:Gene: GDB:GBP1

A:Cross-references: GDB:378351; OMIM:600411

A:Map position: lpter-lqter

C:Superfamily: guanine nucleotide-binding protein 1

Query Match 64.4%; Score 1958.5; DB 2; Length 592;
Best Local Similarity 69.4%; Pred. No. 7.6e-101;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

Qy	1	MALEIHMSDPMCLIFNEQALKVNOEALILSAITQPMVVVAIVGLYRTGKSYLMNKL	60
Db	1	MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKL	60
Qy	61	KNKGFSVASTVQSHTKGIWCVPHNPNHLLVLDTEGLGDVEKADNKNDIQIFALAL	120
Db	61	KNKGFSLSVTSQSHTKGIWCVPHNPNHLLVLDTEGLGDVEKADNKNDIQIFALAV	120
Qy	121	LLSSTFVYNTVNVKIDQAGAILDLHNVTETLLKARNSPD--LDRVDPADSGASFPFDL	178
Db	121	LLSSTFVYNSIGTINQAMQQLYVVTETLTHIRSKSPDENENEVEDSADFSVFPDFV	180
Qy	179	TLRDPFCLGLIDGQLVTPDEYLENSLRPKQSDORQVNFNPLRLCIQKFFPKKCFPDL	238
Db	181	TLRDPFSLDLADGQPLTPDEYLTSLKLGKTSQKDETFLRLCIRKFFPKKCFVDFR	240
Qy	239	PAHQKLAQLLETLPDDLEPEFVQOVTEFCSYIFSHMTKTLPGGIWVNGSRKLNVLTY	298
Db	241	PVHRKLAQLKLEKQDELEPEFVQOVADFCSYIFSNKTKLTSGLIQVNGRPLSLVITY	300
Qy	299	VNAISSGDLFCIENAVILALAQRENSAAVQKAIHYDQMGQKQVLPMTLQELDLHRTS	358
Db	301	VNAISSGDLFCMENAVILALAQIENSAVQKAIHYEQMGQKQVLPMTLQELDLHRTS	360
Qy	359	EREAIEVFMKNSFKVDQSQFQKELETLLDAKQNDICRNLEASSDYCSALLKIDFLGPLEE	418
Db	361	EREAIEVFISSFKVDVHLQFKELAAQLKRRDDFCQKQNSASSDRCSGLLQVIFSPLEE	420

T17320
hypothetical protein DKFZp564J0863.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17320
R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18727
A:Accession: T17320
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-555 <DUE>
A:Cross-references: UNIPROT:Q9UFL1; EMBL:AL117600
A:Experimental source: fetal brain; clone DKFZp564J0863
C:Genetics:
A>Note: DKFZp564J0863.1

Query Match 8.3%; Score 251.5; DB 2; Length 555;
Best Local Similarity 24.9%; Pred. No. 1.2e-06;
Matches 112; Conservative 68; Mismatches 182; Indels 87; Gaps 19;

QY 2 ALRIHSDP--MCLIEFNFNQLKVNQEALIELSAITQ-----PVVVVAIVGLYRGKSY 53
 | | | | :
DB 32 AMESSKPGPVQVVLVKQDHSHFELDEKAL--ASILLQDHIRDLVDVVSVAGAFRKGSF 89
 | | | | :
QY 54 LMN-----KLAGKNK-----GFSVASTVQSHTKGIWIW----CVPHENWNPN 90
 | :
DB 90 ILDFMLRYLYSQESGHSNWLGDPEEPLTGFSWRGGSDPETTGIQIWSSEVFTVEKPGKK 149
 | | | | :
QY 91 HTLVLLDTGLGVGEKADNKNDIQIFALALLLSSTFYNTVNVKIDQGAIDLHNVTETLD 150
 | | | | :
DB 150 VAVVLMDTQAFD--SQSTVKDCAAIFALSTMSTSSVIYNLSQNIQSDDDLQQQLFTEYGR 208
 | | | | :
QY 151 LLKARNSPDLDRV--EDPADSASFDPDLVWTLRDFCLGLEIDGOLVTPDPEVLNSLRPKQG 209
 | :
DB 209 LA-----MDEIFRPK-----FQTLMFIVRDRSPFEYSYSLQGGMAPLDRKLQVKSH 255
 | :
QY 210 SDORVQNFLPRLCIQKFPPKKCFIPDLPAHQKLAQLETLDP-----DELEPEFVOQV 264
 | :
DB 256 QHEEIQNV---RNHIHSCFSDVTCFLPHFG-----LQVATSPDFDGKLKDIAAGEFKQL 307
 | :
QY 265 TEFCSYIFSHMTKTLPGGIM---VNGSR-----LKNLVITYVNAISSGDLPCINAVLA 316
 | :
DB 308 QALIPYYLN-----PSKLMKEINGSKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLOA 360
 | :
QY 317 LAQENSAAVOKAI AHYDOOM-----GQKQVLPMTLOELLDLHRTSEREAIEVFMKN-- 369
 | :
DB 361 TAEAYNLMAAASAKDIYNNMEECVGCEKPYLSPDILEE---KHCEFQKQLADHPHFKTKK 417
 | :
QY 370 -SPKDVDSQSFQKETLLDAKQNDICKRN 397
 | :
DB 418 MGKGDFSFRYQQELEEEIKEELYENFCKHN 446
 | :

RESULT 7
A84810
Probable guanylate binding protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: A84810
R:Liu, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84810
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <STO>
A:Cross-references: UNIPROT:Q8S8C8; GB:AEO02093; NID:g6598487; PIDN:AACT9624.2; GSPDB:GN
C:Genetics:
A:Gene: At2g38840

A;Map position: 2

Query Match 7.1%; Score 216; DB 2; Length 217;
Best Local Similarity 40.9%; Pred. No. 3.5e-05;
Matches 47; Conservative 26; Mismatches 36; Indels 6; Gaps 3;

Qy 20 QLKVNQALBILSAITOPVVVAIVGLYRTGKSYLMNKLAKGN--KGFSVASTVQSHTKG 77
:
Db 28 KLOLSRGLBLAISRIITPIASAVAVIGPYRSKSPFLNQLLSLSCYEFGVGVMHMDTKTG 87
:
Qy 78 IWTWCVP---HPNPWNHTLVLLDTGELGDVEKADKNKDIOIFALALLSSFFVYN 129
:
Db 88 IWNGTPLELEIDGVKTSTVIYLDTEGFESVGKS-NVYDDRIFALATWSSVLIN 141
: :

RESULT 8
H86168
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86168
R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86168
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-991 <STO>
A;Cross-references: UNIPROT:Q9ZWA5; GB:AEO05172; NID:g4204314; PIDN:AAI0695.1; GSPDB:8
C;Genetics:
A;Map position: 1

Query Match 7.0%; Score 213.5; DB 2; Length 991;
Best Local Similarity 18.2%; Pred. No. 0.00032;
Matches 124; Conservative 133; Mismatches 230; Indels 193; Gaps 26;

Qy 18 NEOLKVNOEALILSALTQPVVVAIVGLYRTGSKYLNNKLAKGNKGFSVASTVQSHTKG 77
:
Db 20 NGKLTDPDAIGALKOKGPVAVVSFSGKALQGKSFVFNQLLSRGISGEVOTLHRPCMGD 79
:
Qy 78 IWTWCVP---HPNPWNHTLVLLDTGELGDVEKADKNKDIOIFALALLSSFTVNTVYNK 133
:
Db 80 IWMWIEPVKRISDGTGYSLVLDVE---LEDKSIPTLGNDIAL----- 122
:
Qy 134 IDGAIDLHANVTETDLLKARNSPDLDRVEDPA--DSASFPPDLVTLRFPCGLEIDG 191
:
Db 123 -----DLSRLLEIRKQDHVGEAKDNITFFELGGQSPFMFVQLMMDSINSETVEGG 169
:
Qy 192 QLVTYPD-----EYLENSLRPKOGSD-----ORQNF 217
:
Db 170 EDTVTSNKMLKRLPLYGYDALMKVFYSVRPRKQRGTIVTPPLAGFTKAFSENVNN 229
:
Qy 218 NLPLRC----IQKFPPKKCFIFDLPAHQKLAOLETLPDDLEBP-----FVOQTFFC 268
:
Db 230 IVPKISIMQTVLEGRRARDTATEVYMSSLERSET-PDESMLEAHNKAVVEALTAF 288
:
Qy 269 SYIFSHSMTKTLPGGIWNGSRNLKNLVLYVNAISSGD----- 306
:
Db 289 -----ESSIGNVEVKQYKRDLSFFAKALEDHKRVANVEAYSRCCNAIEDMGKKL 339
:
Qy 307 --LPCIENAVLALAQRSNAVQKAIAHYDOOMG-----QKV-QLPMETLOELLDLHETS 358
:
Db 340 WALPFCSDANIG----DMIKALDTAVAEYEASINGPMKWQKLSFLRESVDAIL-VHRRG 394
:
Qy 359 -----EREATIEVFMKNSFKVD-----QSPQKELETLLDKAQNDICRN 397
: :

A;Gene: CESP:F48F5.1
A;Map position: 5
A;Introns: 753/2; 814/3; 987/2; 1030/3; 1114/2; 1153/3; 1222/3
Query Match 5.3%; Score 160.5; DB 2; Length 1291;
Best Local Similarity 18.7%; Pred. No. 0.38;
Matches 143; Conservative 100; Mismatches 224; Indels 299; Gaps 31;
QY 14 IENFNEOLK-----VNQEALEILSALTQPVVVVAIVGLYRGTCKSVLNMKLAG 60
DB 287 LSRVNEKLKSTTPADNARQVSNQFKESFSVPTDAVSAVGLABYKK-----CNHLGG 341
QY 61 -----KNKGFSVASTVQSHGTGIWICVPHENPNHTLVLL-----DTEGLGDEKADNK 110
DB 342 PQTDDERRPGHEPMKVK-----VGDLSIALHMFQTLALQOLEK-----382
QY 111 NDIQIFALAL-----LLSSTFVYNTVYVNAISGDLPFCIENAVLALQRENSAIVKAIH 160
DB 383 -DVADPVKSLTFTDINNQTLSGEIVKVVVEDIKKSGKLAKIQBNVKSIEDKINGIKLKNL 441
QY 161 DRVEDPADSASFPFDLWTLRDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQVQNFNLP 220
DB 442 ESTLLENLANSFTQDVMFK-----EVITAEVSG-----471
QY 221 RLCIOKFFPKKCFIFDLPAHOKKLAQLETLDPDELEPEFVQOVTFCYSIFSHSM--TK 278
DB 472 --CLQK-LKAKSLVLTQATATQIKRLK-----DDKL-LESVQQTAKSVSQ-FSETLASVK 522
QY 279 TLPGGIMVNGSRLLKLVLYVYVNAISSGDLPCFICINAVLALQRENSAIVKAIH 332
DB 523 KIPDAMKKN-----VKNVTLELNKRSESLNQSDAISHSASALR 560
QY 333 -----YQQMQG-----KVQLPME--TLQELLDLHRTS--EREALTEVFMK 368
DB 561 SVFGLVKLESSIGQLNDTPTIVSSIEDKIKIPAEKMKLQKMGNHTGEMVSLQAAVVQAK 620
QY 369 NSFQKVDQS-----FQKELETLLDAKQ-----390
DB 621 AFVAKIDVSKLTLNYSAILKTLTPDVPVMEALSEVLEILIRAI SATRRRRRAAG 680
QY 391 -----NDICKRNLEASSDYC-----SALKDITGPLEBAVKQGIYS 426
DB 681 SNAHLVAAKVILDKIAALDLQFSSNIAHFKNAPLAFQSFSKLAKFF-----ATQCKISA 735
QY 427 KPGG-----HNLF 435
DB 736 SQNGGGGGGGSEFPFTVIVVSVIVGALLLALAAFLAVLVYGFHQRKQAKIDRDNKEI 795
QY 436 QKTEELKAKYRPRKGIQAE--VLQKYLKSESVSHAI-----LQTDQAL 480
DB 796 RDEIENARQAEENEORIAAEKNALEAKIKEKSNMRKVDEQNQRKDELOAKLRADQEK 855
QY 481 TETEK-----KKKEAQVKAFAEKAQRLAAIQRNEQMMQERLHQBQVROM 529
DB 856 SEARKIAEKKKDEQNKKEAKLRADQEKSEARKVAE--KKKDEQNKEDKQLQAKLRADQ 914
QY 530 EIAKQNWLABQKQKQOQVQVFNCP--ISPLP-VTMVRCSSGKEG 572
DB 915 EKSEARKIAEKKKKEDEAKQVKNWIKMKMFTTLRACADPIEG 960
RESULT 12
T13030
microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13030
R;Lant, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
A;Title: A class VI unconventional myosin is associated with a homologue of a microtubul
A;Reference number: Z17588; MUID:98139549; PMID:9472041
A;Accession: T13030
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1690 <LAN>
A;Cross-references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1
A;Experimental source: strain Oregon R
C;Genetics:
A;Cross-references: FlyBase:FBgn0020503
C;Keywords: cytoskeleton
Query Match 5.3%; Score 160.5; DB 2; Length 1690;
Best Local Similarity 20.8%; Pred. No. 0.54;
Matches 114; Conservative 90; Mismatches 185; Indels 159; Gaps 26;
QY 104 VEKADNKDQIFALALLLSSTFVYNTVYVNAISGDLPDQGAIDL---LHNVTELTDLKARNSPDL 160
DB 385 VERDLDRDQAQNALQ-----QKNINELKARIVELESALGNRKKTEELQC-----SI 433
QY 161 DRVEDPADSASFPFDLWTLRDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQVQNFNLP 220
DB 434 DEAQ-----FC-GDELNAQSVYKEKIH-----LESKITKLVA 467
QY 221 RLCIOKFFPKKCFIFDLP---AHOKKLAQLE---TLPDDLEPEFVQO-----VTFF 267
DB 468 TPLSQILPP-----DLPDGDALQSEIAQIQEKMTIQOKEVESRIASQLEEBQRLRN 521
QY 268 CSYIFSHMTKTLPGGIMVNGSRLLKLVLYVYVNAISSGDLPC-IEN--AVLALQRENSA 324
DB 522 VKYL--NEQIATLQSELVSKDEALEKFSLS-----ECGIENLRRELALLKEENEK 569
QY 325 AVQKAIHYDQMGQKQVLPMTLQELLDLHRTS---EREAL-----EVPKKN- 369
DB 570 QAQEAQAEPTRLAEKSEVLRSLSELQNLKATSDLESERVNKSDECEILOTEVMRDE 629
QY 370 SPKVDVDSQKLETLTLLDAKQNDICKRNLEASSDYCSALLKIDIFGLPEBAVKQGIYSKPG 429
DB 630 QIRELNQQLD-EVTTQLNVQKAD-----SSALDDML-----RLQKEGTEEK-- 669
QY 430 GHNLFQKTEELKAKYRPRKGIQAEVLOKYLK-----464
DB 670 --STLLEKTEKELVQIKEQAATLQDKEQLQISDLKQLARQEKLVREKTENAINQIQ 727
QY 465 SKESVSHAILQTDQALTETETKTKKKAQVKAFAEKA--AORLAAIQRNEQ 513
DB 728 EKESIEQQLALKQNELEDPFQKQSESEVHLQBIKAQNTOKLELVESGESLKKLOQLEEB 787
QY 514 MMQERLHQBQVROMWEIAKQNWLABQKQKQV--QQQVQVFNCFISPLPT-----NR 564
DB 788 KTLGHEKL---QAALTEELKKEKETIKKEQBELQQLQSKSABSESALKVQVQLEQLQQ 844
QY 565 VCSSGKEG 572
DB 845 AAASGEEG 852
RESULT 13
A39638
plectin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A39638; S21876
R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Stratow
J. Cell Biol. 114, 83-99, 1991
A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with
A;Reference number: A39638; MUID:91268156; PMID:2050743
A;Accession: A39638
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-4687 <WIC>
A;Cross-references: UNIPROT:P30427; EMBL:X59601; NID:g1292885; PIDN:CAA42169.1; PID:g15
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein
C;Keywords: cytoskeleton; transmembrane protein
F;6-103/Domain: ribosomal protein S10 homology <RS10>
F;184-399/Domain: alpha-actinin actin-binding domain homology <ACT>

Qy	182	DFCLGLEIDQQLVTPDEYLENSL	-----RPKQGSDDORVQNFNLPRLCIQKFFP	229
Db	194	DH-IG-----VTPLANLNTLIQDLTHIWSSISKPAGLENSKIEDY	-----	233
Qy	230	KKKCFIPDLPAHOKKLAQLETLDPDBLEPFVQVTEFCYSYIFSHSMWTKLPGGIMWNGS	289	
Db	234	-----FQFAALPHKILQ-----PD-----KFISEVQNL-----GSRFTIAGH	266	
Qy	290	RLKNLVITYVNAISSGDLPCIEANVLALAQRENSAAVQKAIAHYDQMGQKQVQLPMETLQ	349	
Db	267	RNKD-----SDATDQELTGGVFLP-----	286	
Qy	350	ELLDLHRTSREAEIVFMKN-----SFKDVDSFOKELETLTLLDAQNODICKENLEASSD	403	
Db	287	---EYHRRIPADGLSIVAEIGWDQIVSNKDLPLTQOE---LLAQFCDIEAREVQIAFD	340	
Qy	404	YCSALLKDIPIGPLEEAVKQGIYKPG-----GHNLFIQKTEELKAKYYR--EPRKGIQAE	456	
Db	341	AAIAPLEEQAESTRACKPAVLNQLGIGAEAREKCVKNFETQASRYHKGVYTKRAELE	400	
Qy	457	EVLQKYLS-----KESVSHAILQTDQA-----LTETETKKKKEAQ	491	
Db	401	DKIDNRLKALYQAHLTAAHKAGVTAPEAVANAVKAGQAGGAYFAEIVKEQKTKTLEI	460	
Qy	492	VKAEEAKAEQRLAAIQRONEQNMQRE-----RLHQEVROMETAKONWLAEQOQKMQE	545	
Db	461	FKKEAQSLAIPGVAMSNFKPYQILFEKELDEVSARLRKEMRLAIRVERWVKSR-----	515	
Qy	546	QMQVFINCFISPLPYTMRVSSGKSGEAAARSCG-----SQQGVWSQKVM	590	
Db	516	-----LGDAIGLEFNKLGSRGSGAPESGEKPAEKDIW-DRVM	554	

RESULT 15

H90279
microtubule binding protein, probable [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90279
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.;
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; I-
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90279
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <KUR>
A:Cross-references: UNIPROT:Q9UXN4; GB:AE006641; NID:gl3814451; PIDN:AAK41495.1
C:Genetics:
A:Gene: SSO1256

Query Match 5.2%; Score 158; DB 2; Length 464;
Best Local Similarity 23.0%; Pred. No. 0.14;
Matches 85; Conservative 81; Mismatches 136; Indels 68; Gaps 17;

Qy	251	LPDEL-----EPEFVQVTEFCYSYIFSH---SMWTKLPGGIMVNGSRLLKNLVLYTVNAI	302	
Db	2	LKDDILKLKLEDAEFKQVVEETILGISFINVTLADLKILKLLASMDKLKSLVDQLVDAQ	61	
Qy	303	SSGD--LPCIENAV--LALAORENSAAVQKAIAHYDQMGQKQVQLPMETLQELDLHRTS	358	
Db	62	RRAEERIAKLENAVEQLVSAQKRTDBRITKL-----EESTKKLE---QAVQELIEAQKKH	113	
Qy	359	EREAEIVFMKNSPKVDQSFQKELETLTLLDAQNODICKENLEASSDSCSALLKDIQFPLEE	418	
Db	114	DERITK--LEESTKKLEQAVQELIEA---QKHDERITKLESTK-----KLEQ	157	
Qy	419	AVKQGIYSKPGGHNLFIQKTEELKAKYREPRKGIQAEVQLKYLSKESVSHAILQTDQ	478	
Db	158	AVQELIEAQK-KHDERITKLEESTKKLEQAVQELIEAOKKHDERITKLESTKKLEQAVQ	216	

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QY 479 ALTETEKKKE-----AQVKAEEKAEQRLAAIAIORQNEQMMQERERLHQ 523
Db 217 ELIEAQKKHDERITKLEESTKKLEQAVQBLIEAQKKHDERITYKLE-ESIQKLVDAQRRAE 275
QY 524 EQVRQMEIAKQNWLAEQQKMQEQMVFQNCFISPL-PVTMRVCSS--CKEG---EAARS 577
Db 276 ERIAKLENAVEQ-LVEAQKRTDER-----ITKLEEVTKLVESQLGMQNEIRELRKA 326
QY 578 CGSQQGVWSQ 587
Db 327 LGSMDGKRWGR 336
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Search completed: May 20, 2005, 13:28:53
Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2005, 13:21:01 ; Search time 179 Seconds
(without alignments)
1690.720 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHMSDPMLLIENFNEQ.....GEAARSCGQGVMSQKVVV 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2815	92.5	586	1	Q96pp8 homo sapien
2	2516	82.7	489	2	Q86tms homo sapien
3	2490	81.8	504	2	Q8nf03 homo sapien
4	2236	73.5	481	2	Q8n404 homo sapien
5	1958.5	64.4	592	1	Q8p1 HUMAN
6	1933	63.5	724	2	Q8bm77 mus musculus
7	1907.5	62.7	590	1	Q8cfb4 mus musculus
8	1905.5	62.6	561	2	Q8bu78 mus musculus
9	1897	62.3	591	1	Q8p2 HUMAN
10	1892	62.2	591	2	Q8p2 HUMAN
11	1774.5	58.3	563	2	Q8h0r5
12	1765.5	58.0	589	1	Q8p1_MOUSE
13	1764	58.0	481	2	Q8p1_MOUSE
14	1757.5	57.8	589	1	Q8p2 RAT
15	1750.5	57.5	589	1	Q8p2_MOUSE
16	1528.5	50.2	638	2	Q8n8v2
17	1510.5	49.6	633	2	Q8zn66
18	1500.5	49.3	640	1	Q8p4 HUMAN
19	1498.5	49.2	640	2	Q8nsl0
20	1493.5	49.1	633	2	Q7z3f0
21	1482.5	48.7	638	2	Q8bu48
22	1482.5	48.7	641	2	Q8kan1
23	1479.5	48.6	632	2	Q81z40
24	1468.5	48.3	620	2	Q8vec5
25	1459.5	48.0	620	2	Q81107
26	1407	46.2	612	2	Q8cfa8
27	1392.5	45.8	611	2	Q8zql8
28	1388.5	45.6	447	2	Q8nv33
29	1377.5	45.3	611	2	Q8p2n2
30	1365.5	44.9	623	2	Q61594
31	1344	44.2	619	2	Q6pg83

32	1342.5	44.1	595	2	Q6gn80
33	1335	43.9	619	2	Q8bts3
34	1333	43.8	587	2	Q6dpg7
35	1325.5	43.6	607	2	Q7t0s6
36	1259	41.4	620	2	Q66j21
37	1229.5	40.4	528	2	Q66ir9
38	1198	39.4	635	2	Q8lyl1
39	1183	38.9	621	2	Q6dhp7
40	1148.5	37.7	385	2	Q8k0g1
41	1097	36.0	290	2	Q6p3v3
42	1054	34.6	576	2	Q90892
43	886	29.1	744	2	Q8p2c12
44	614.5	20.2	380	2	Q7tmv8
45	587.5	19.3	374	2	Q66k09

ALIGNMENTS

RESULT 1
ID GBPS HUMAN STANDARD; PRT; 586 AA.
AC Q96pp8;
DT 29-MAR-2004 (Rel. 43, Created)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon-induced guanylate-binding protein 5 (GTP-binding protein 5)
DE (Guanine nucleotide-binding protein 5) (GBP-TA antigen)
DE (UNQ2427/PRO4987).
GN Name=GBP5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]_taxid=9606;
RP SEQUENCE FROM N.A.
RA Avdalovic A., Fu H., Tsurushita N.;
RT "Human GBP-4 and -5: new members of the IFN-gamma-inducible guanylate-binding protein family";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Eichmueller S., Hartmann T., Thiel D., Usener D., Dummer R., Schadendorf D.;
RT "GBP-TA: a new tumor-specific antigen of cutaneous lymphoma depicted by serological detection";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yanagita D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=22338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywiniski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- SIMILARITY: Belongs to the GBP family.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
DR EMBL; AF288815; AAL02055.1; -;
DR EMBL; AF430642; AAN39035.1; -;
DR EMBL; AF430643; AAN39036.1; -;
DR EMBL; AY358953; AAO89312.1; -;
DR EMBL; BC031639; AAH31639.1; -;
DR HSSP; P32455; 1DG3.
DR Genew; HGNC:19895; GBP5.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02263; GBP; 1.
DR GTP-binding; Lipoprotein; Multigene family; Prenylation.
KW NP_BIND 45 52 GTP (By similarity).
FT NP_BIND 97 101 GTP (By similarity).
FT LIPID 583 583 S-geranylgeranyl cysteine (By
similarity).
SQ SEQUENCE 586 AA; 66617 MW; 95DDC02F0FB705D0 CRC64;
Query Match 92.5%; Score 2815; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.7e-134;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGGFSVASTVQSHYGTGIWICVPHNPWNHNTLVLLDTGLGDKVEKADNKNDIQIFALAL 120
DB 61 KNGGFSVASTVQSHYGTGIWICVPHNPWNHNTLVLLDTGLGDKVEKADNKNDIQIFALAL 120
QY 121 LLSSTFVYNTVANKIDQAGIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDLVWTL 180
DB 121 LLSSTFVYNTVANKIDQAGIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDLVWTL 180
QY 181 RDFCLGLEIDGQVLTDPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 181 RDFCLGLEIDGQVLTDPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
QY 241 HQKLAQLETLPPDELEPEFVQVTFCSYIFSHSMTKTLPGIMWNGSLKRLNVLTYVN 300
DB 241 HQKLAQLETLPPDELEPEFVQVTFCSYIFSHSMTKTLPGIMWNGSLKRLNVLTYVN 300
QY 301 AISSGDLPCLENVLAQENSAVQKAIHAYDQMGKQVQLPMETQLQELLDLHRTSER 360
DB 301 AISSGDLPCLENVLAQENSAVQKAIHAYDQMGKQVQLPMETQLQELLDLHRTSER 360
QY 361 EAEIVFMKNSFKVDQDSFOKELETLLDAKQNDICKRNLEASSYCSALLKDIIFGPLEEAV 420
DB 361 EAEIVFMKNSFKVDQDSFOKELETLLDAKQNDICKRNLEASSYCSALLKDIIFGPLEEAV 420

QY 421 KQGYSPGPGHNLFIQKTEELKAKYRPRKGIQAEVQLKYLKSKESVSHAILQTDQAL 480
DB 421 KQGYSPGPGHNLFIQKTEELKAKYRPRKGIQAEVQLKYLKSKESVSHAILQTDQAL 480
QY 481 TETEKKEAQAQKAEAEKAEQAQRLAAIQORNEQWQERERLHQBQVROMETAKQNLAEQ 540
DB 481 TETEKKEAQAQKAEAEKAEQAQRLAAIQORNEQWQERERLHQBQVROMETAKQNLAEQ 540
QY 541 QKMQEQQMQ 549
DB 541 QKMQEQQMQ 549
RESULT 2
Q86TMS PRELIMINARY; PRT; 489 AA.
ID Q86TMS
AC Q86TMS;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE CTCL tumor antigen GBP-5ta (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cutaneous lymphoma;
RX PubMed=14996095;
RA Hartmann T.B., Thiel D., Dummer R., Schadendorf D., Eichmuller S.;
RT "SEREX identification of new tumour-associated antigens in cutaneous
T-cell lymphoma.";
RL Br. J. Dermatol. 150:252-258 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cutaneous lymphoma;
RX PubMed=15175044;
RA Fellenberg F., Hartmann T.B., Dummer R., Usener D., Schadendorf D.,
RA Eichmuller S.;
RT "GBP-5 splicing variants: New guanylate-binding proteins with tumor-
associated expression and antigenicity.";
RL J. Invest. Dermatol. 122:1510-1517 (2004).
DR EMBL; AF328727; AAO40731.1; -;
DR HSSP; P32455; 1DG3.
DR GO; GO:0005525; F-GTP binding; IEA.
DR GO; GO:0003924; F-GTPase activity; IEA.
DR GO; GO:0006955; P-immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02263; GBP; 1.
DR NON_TER 489_489
FT SEQUENCE 489 AA; 55247 MW; B493C3586DFFDA1D CRC64;
Query Match 82.7%; Score 2516; DB 2; Length 489;
Best Local Similarity 99.8%; Pred. No. 1.8e-119;
Matches 488; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGGFSVASTVQSHYGTGIWICVPHNPWNHNTLVLLDTGLGDKVEKADNKNDIQIFALAL 120
DB 61 KNGGFSVASTVQSHYGTGIWICVPHNPWNHNTLVLLDTGLGDKVEKADNKNDIQIFALAL 120
QY 121 LLSSTFVYNTVANKIDQAGIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDLVWTL 180
DB 121 LLSSTFVYNTVANKIDQAGIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDLVWTL 180
QY 181 RDFCLGLEIDGQVLTDPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 181 RDFCLGLEIDGQVLTDPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240


```
Qy 241 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 300
Db 241 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 300
Qy 301 AISSGDLPCIEENAVLALAQRENSAAVQKAIHAHYDOQMGQKQVQLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCIEENAVLALAQRENSAAVQKAIHAHYDOQMGQKQVQLPMETLQELLDLHRTSER 360
Qy 361 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICRNLKRNLEASSDYCSALLKDI FGPLEBAV 420
Db 361 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICRNLKRNLEASSDYCSALLKDI FGPLEBAV 420
Qy 421 KOGIYSPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KOGIYSPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Qy 481 TETKKKKE 489
Db 481 TETKKKKE 489
```

RESULT 3

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Q8NF03 Q8NF03 PRELIMINARY; PRT; 504 AA.
AC Q8NF03;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE FLJ00401 protein (Fragment).
GN Name=FLJ00401;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090479; BAC03460.1; -.
DR HSSP; P32455; 1DG3.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:Immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP_C; 1.
FT NON_TER 1
FT NON_TER 504
SQ SEQUENCE 504 AA; 56862 MW; 37E814E34539F743 CRC64;
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Query Match 81.8%; Score 2490; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.9e-118; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALBIHSDPNCMLIENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Db 22 MALBIHSDPNCMLIENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 81
Qy 61 KNGFSVASTVQSHTKGIWICVPHNPWNTLVLLDTEGLGDVEKADKNKNDIQIFALAL 120
Db 82 KNGFSVASTVQSHTKGIWICVPHNPWNTLVLLDTEGLGDVEKADKNKNDIQIFALAL 141
Qy 121 LLSSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 142 LLSSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVWTL 201
Qy 181 RDFCLGLEIDQLVTPDEYLENSLRPKQSDQRVQNFNLPRLCIQKFPFKKCFIFDLPA 240
Db 202 RDFCLGLEIDQLVTPDEYLENSLRPKQSDQRVQNFNLPRLCIQKFPFKKCFIFDLPA 261
Qy 241 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 300
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Db 262 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 321
Qy 301 AISSGDLPCIEENAVLALAQRENSAAVQKAIHAHYDOQMGQKQVQLPMETLQELLDLHRTSER 360
Db 322 AISSGDLPCIEENAVLALAQRENSAAVQKAIHAHYDOQMGQKQVQLPMETLQELLDLHRTSER 381
Qy 361 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICRNLKRNLEASSDYCSALLKDI FGPLEBAV 420
Db 382 EAIEVFMKNSFKVDQSFQKELETLDDAKQNDICRNLKRNLEASSDYCSALLKDI FGPLEBAV 441
Qy 421 KOGIYSPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Db 442 KOGIYSPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 501
Qy 481 TET 483
Db 502 TET 504
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RESULT 4

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Q8N4Q4 Q8N4Q4 PRELIMINARY; PRT; 481 AA.
AC Q8N4Q4;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Similar to guanylate binding protein 5 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033761; AAH33761.1; -.
DR HSSP; P32455; 1DG3.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:Immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP_C; 1.
FT NON_TER 1
FT NON_TER 481
SQ SEQUENCE 481 AA; 55070 MW; 3E642C58BCA06895 CRC64;
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Query Match 73.5%; Score 2236; DB 2; Length 481;
Best Local Similarity 99.8%; Pred. No. 2.6e-105;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 110 KNDIQIFALALLISSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADS 169
Db 5 KNDIQIFALALLISSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADS 64
Qy 170 ASFPDPLVWTLRDPCLGLEIDQLVTPDEYLENSLRPKQSDQRVQNFNLPRLCIQKFPF 229
Db 65 ASFPDPLVWTLRDPCLGLEIDQLVTPDEYLENSLRPKQSDQRVQNFNLPRLCIQKFPF 124
Qy 230 KKCFIFDLPAHQKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGS 289
Db 125 KKCFIFDLPAHQKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGS 184
Qy 290 RLKLNVLTYNATSSGDLPCIEENAVLALAQRENSAAVQKAIHAHYDOQMGQKQVQLPMETLQ 349
Db 185 RLKLNVLTYNATSSGDLPCIEENAVLALAQRENSAAVQKAIHAHYDOQMGQKQVQLPMETLQ 244
Qy 350 ELLDLHRTSREATEVFMKNSFKVDQSFQKELETLDDAKQNDICRNLKRNLEASSDYCSALL 409
Db 245 ELLDLHRTSREATEVFMKNSFKVDQSFQKELETLDDAKQNDICRNLKRNLEASSDYCSALL 304
Qy 410 KDIFGPLEBAVQKGIYSPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESV 469
```

Db 305 KDIFGPLEEAVKQGIYKPGKHNLFTQKTEELKAKYVRPRKGIQAEVLYKYLKSKESV 364

Qy 470 SHAIIQTQDALTEKTEKKKEAQVKAFAEAKAQRLLAAIORONEQMMQERERLHQEQVROM 529

Db 365 SHAIIQTQDALTEKTEKKKEAQVKAFAEAKAQRLLAAIORONEQMMQERERLHQEQVROM 424

Qy 530 EIAKQNLWLAEQKMQEQQQQ 549

Db 425 EIAKQNLWLAEQKMQEQQQQ 444

RESULT 5

GBPI_HUMAN

ID GBPI_HUMAN STANDARD; PRT; 592 AA.

AC F32455;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1)

DE (Guanine nucleotide-binding protein 1) (hUGBP-1).

GN Names=GBPI;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RX MEDLINE FROM N.A.

RX MEDLINE=91342675; PubMed=1715024;

RA Cheng Y.-S.E., Patterson C.E., Staeheli P.;

RT "Interferon-induced guanylate-binding proteins lack an N(T)KXD

RT consensus motif and bind GMP in addition to GDP and GTP.;"

RL Mol. Cell. Biol. 11:4717-4725(1991).

RN [2]

RP SEQUENCE FROM N.A.

RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,

RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,

RA Phelan M., Farmer A.;

RT "Cloning of human full-length CDSs in BD Creator(TM) system donor

RT vector.;"

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.;"

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [4]

RP ISOPRENOL.

RX MEDLINE=96427476; PubMed=8830800;

RA Nantais D.E., Schwenmle M., Stickney J.T., Vestal D.J., Buss J.E.;

RT "Prenylation of an interferon-gamma-induced GTP-binding protein: the

RT human guanylate binding protein, huGBPI.;"

RN [5]

RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

RX MEDLINE=20140138; PubMed=10676968; DOI=10.1038/35000617;

RA Prakash B., Praecke G.J.K., Renault L., Wittinghofer A., Herrmann C.;

RT "Structure of human guanylate-binding protein 1 representing a unique

RT class of GTP-binding proteins.;"

RL Nature 403:567-571(2000).

CC -!- FUNCTION: Binds GTP, GDP and GMP.

CC -!- INDUCTION: By interferon gamma during macrophage activation.

CC -!- SIMILARITY: Belongs to the GBP family.

CC

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CC or send an email to license@isb-sib.ch).

CC

CC EMBL; M55542; AAA35871.1; -.

DR EMBL; BT006847; AAP35493.1; -.

DR EMBL; BC002666; AAH02666.1; -.

DR EIR; A41268; A41268.

DR PDB; 1DG3; X-ray; A=1-592.

DR PDB; 1F5N; X-ray; A=1-592.

DR Genew; HGNC:4182; GBPI.

DR H-InvDB; HIX0018119; -.

DR MIM; 600411; -.

DR CO; GO:0005525; F:GTP binding; TAS.

DR InterPro; IPR003191; GBP.

DR Pfam; PF02263; GBP; 1.

DR Pfam; PF02841; GBP C; 1.

KW 3D-structure; GTP-Binding; Interferon induction; Lipoprotein;

KW Multigene family; Polymorphism; Prenylation.

FT NP_BIND 45 52 GTP.

FT NP_LIPID 97 101 S-farnesyl cysteine.

FT LIPID 599 589 S -> T (in dbSNP:1048425).

FT VARIANT 349 349 /FTID=VAR_014849.

FT

FT STRAND 11 17

FT TURN 18 19

FT STRAND 20 23

FT HELIX 25 32

FT TURN 33 33

FT STRAND 37 46

FT TURN 47 48

FT HELIX 51 58

FT TURN 59 60

FT STRAND 78 84

FT TURN 89 90

FT STRAND 92 98

FT STRAND 101 101

FT HELIX 104 106

FT TURN 110 111

FT HELIX 112 122

FT STRAND 125 131

FT HELIX 136 140

FT TURN 141 142

FT HELIX 143 146

FT TURN 147 147

FT HELIX 148 151

FT STRAND 153 153

FT HELIX 167 170

FT HELIX 171 174

FT STRAND 177 183

FT TURN 184 184

FT HELIX 198 205

FT TURN 206 206

FT HELIX 214 229

FT STRAND 233 237

FT HELIX 244 252

FT HELIX 255 257

FT HELIX 260 276

FT STRAND 281 282

FT TURN 283 285

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FT STRAND 286 287
FT STRAND 289 289
FT HELIX 290 306
FT TURN 307 307
FT STRAND 311 311
FT STRAND 312 342
FT HELIX 313 371
FT HELIX 350 371
FT HELIX 376 378
FT HELIX 379 423
FT TURN 424 427
FT TURN 430 431
FT HELIX 432 449
FT TURN 455 456
FT HELIX 457 467
FT TURN 468 468
FT HELIX 469 478
FT HELIX 484 563
FT TURN 564 564
FT HELIX 566 582
SQ SEQUENCE 592 AA; 67902 MW; FC05D1B0FB635467 CRC64;

Query Match 64.4%; Score 1958.5; DB 1; Length 592;
Best Local Similarity 69.4%; Pred. No. 3.6e-91;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

QY 1 MALEHMSDPMCLIFNFNEQKVNQAELEILSAITQPVVVAIVGLYRTGKSYLWKLKLAG 60
Db 1 MASEHMTGPMCLIENTNGRLMANPEALKILSAITQPVVVAIVGLYRTGKSYLWKLKLAG 60
QY 61 KNGGFSVASTVQSHTKGIWICVPHNPHTLVLLDTTEGLGDVEKADNKNQDIQIFALAL 120
Db 61 KKGGSFSGTSVQSHTKGIWMCVPHPKPGHILVLLDTTEGLGDVEKADNKNQDIQIFALAV 120
QY 121 LLSSTFVNTVNTKIDOGAIDLLHNVTETDILLKARNSPD--LDRVEDPADSAPFPDLAV 178
Db 121 LLSSTFVNTSNTQINQAMQDLYVTELTIRKSSPDENEVEVSADFSVFPDFVW 180
QY 179 TLRDFCLGLEIDGQAVTPEYLENSLRPKQSDQVRQVNFNPLRCLQIKFFPKKCKCIFDL 238
Db 181 TLRDFSLDLADGQPLTPEYLYTSLKLGKTSQKDETFLNPLRCLIRKFFPKKCKCFVDR 240
QY 239 PAHQKLAQLETLDPDELEPFVQVTFECSYIFSHSMTKLPGLGIMVNGSRLLKNLVUTY 298
Db 241 FVHRKLAQLEKLDDELDPEFVQVADFCYSYFNSNKTTLGSGIQVNGPRLESVLTY 300
QY 299 VNAISSGDLPCENAVLALADRENSAAVOKAIAHYDQMGOKVOLPMETLOELLDLHRTS 358
Db 301 VNAISSGDLPCENAVLALAQIENSAAVOKAIAHYEQMGOKVQPTESLQELLDLHRTS 360
QY 359 EREAIEVPMKNSFKVDVQSFQKLETLDLADKONDICRKNLEASSDYCSALLKIDIFGPLEE 418
Db 361 EREAIEVFISSFKVDVHLFQKELAAQLEKKRDDFCQKQNEASSDRCSGLLQVIFSPLEE 420
QY 419 AVKQGIYKPGCHNLFIOKTELBKAYRPRKGIQABEVLOKYLKSVSHAILQTDQ 478
Db 421 EVKAGIYKPGGYRLFVQKLDLKKYEEPRKGIQABEILQTLKSKESMTDAILQTDQ 480
QY 479 ALTETEKKKKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAE 534
Db 481 TLTEKEKEIEVERKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAE 540
QY 535 NWLAEEQ-----KMQEEQ 547
Db 541 QLLKEQERTLALKQEEQ 558

RESULT 6
Q8BMN7
ID Q8BMN7 PRELIMINARY; PRT; 724 AA.
AC Q8BMN7;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
```

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DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length
DE enriched library, clone:5330409J06 product:weakly similar to GUANYLATE
DE BINDING PROTEIN 5.
GN Name=Gbp5;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipette sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Itoh Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kohji Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sekazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK030414; BAC26953.1; -
DR HSSP; P32455; 1DG3.
DR MGD; MGI:2429943; Gbp5.
DR GO; GO:000525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
```

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DR GO: 0006955; P: immune response; IEA.
DR InterPro: IPR003191; GBP.
DR Pfam: PF02263; GBP_C; 1.
DR Pfam: PF02841; GBP_C; 1.
SQ SEQUENCE 724 AA; 80410 MW; 799C517B51DBF47C CRC64;

Query Match 63.5%; Score 1933; DB 2; Length 724;
Best Local Similarity 64.9%; Pred. No. 8.e-90;
Matches 392; Conservative 70; Mismatches 126; Indels 16; Gaps 5;

QY 1 MALEIHMSDPMCLIEFNQKVNQALFSLAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 KNGKFSVASTVQSHTKGIWICVPHNPNHTLVLLDTGLGDKVEKADKNNDIQIFALAI 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 KNGKFSVASTVQSHTKGIWICVPHNPNHTLVLLDTGLGDKVEKADKNNDIQIFALAI 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LLSSTFVYNTVTKIDQAGIDLLHNVTETLLKARNSPDLDRV--EDPADSASFPFDLVW 178
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LLSSTFVYNTVTKIDQAGIDLLHNVTETLLKARNSPDLDRV--EDPADSASFPFDLVW 179
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 179 TLRFDFGLGIDQLVTPDEYLENSLRPKQSGDQVRQNFNLRCLQKFFPKKCFIFDL 238
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 TLRFDFGLGIDQLVTPDEYLENSLRPKQSGDQVRQNFNLRCLQKFFPKKCFIFDL 239
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 239 PAHOKKLAQLETLPPDELEPEFVQVTEPCSYIFSHMTKTLPGGIWNGSRKLNVLTY 298
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 PALGSKLSQLPTLSNELNSDFVQDLSFCDSHIFTQSKTKTLPGGIQVNGPRLESVLTY 299
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 299 VNAISSGDLPCINAVLAAQRENSAAVOKAIAHYDQOGKQVQLPMETLQELDLHRTS 358
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 VDAINSGLPSTIVVTTLARRENSAAVOKAIAHYDQOGKQVQLPMETLQELDLHRTS 359
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 EREAIEFVKNKSPKVDQSFQKLETLDAKQNDICKRNLEASDYCSALLKIDIFGLPEE 418
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 EREAIEFVKNKSPKVDQSFQKLETLDAKQNDICKRNLEASDYCSALLKIDIFGLPEE 419
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 419 AVKQGIYKPGHNLFIQTEELKAKYRPRKGIQAEVLQKYLKSKESVSHALITDQ 478
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 EVAQEFYHFGGKFLQRMQELKANYRQPGKGTQAEVLQKYLKSKESVSHALITDQ 479
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 479 ALTETKKEKKAQVKAQAEKAEQALAAIQORQNEQMMQRERLHQRVQRMETAKQWLA 538
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 480 VLTDKIQSKAEQERAEARLEAQLAEIRIQEQKAEKAEKAEKAEKAEKAEKAEKAE 539
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 539 EQQKMQEQQMQ-----VFINCPIFSL-----PVTMRVCSGKGEKGAARS 587
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 540 EQQKMQEQQMQ-----VFINCPIFSL-----PVTMRVCSGKGEKGAARS 597
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 588 KVVW 591
Db |||:
QY 598 ALWI 601
Db |||:

RESULT 7
GBP5_MOUSE STANDARD; PRT; 590 AA.
ID GBP5_MOUSE AC Q8CFB4; Q8CFB4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon-induced guanylate-binding protein 5 (GTP-binding protein 5)
DE (Guanine nucleotide-binding protein 5) (MuGBP-5).
GN Name=GBP5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RC MEDLINE=22284156; PubMed=12396730; DOI=10.1089/107999002760274926;
RX
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Db 121 LLSSTFVNTWKNIDQGAIDLHNVTELTDLTRKNSDSNQTEGEPAD-MSFFPDLVW 179
Qy 179 TLRDFCLGLEIDGQAVTTPDEYLENSLRPKQSDQDVQVNFNLRCLQKFFPKKCFIDL 238
Db 180 TLRDFCLDQANGHAITSDEYLENSLRPKQSDQDVQVNFNLRCLQKFFPKKCFVDA 239
Qy 239 PAHQKLAQLETLDPDELEPFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVITY 298
Db 240 PALGSKLSQLETLNNEELNSDFVQDLSEFCSHIFTQSKTKTLPGGIVNGPRLSLVITY 299
Qy 299 VNATSSGDLPCENAVLALAQRENSAAVQKAIAHYDQMGQKVOLPMETLOELDLHRTS 358
Db 300 VDAINSGLPSEIENVTLARRENSAAVQKAIAHYDQMSKQVLTPTTLOELDLHRTC 359
Qy 359 EREAIEFPMKNSFDVDSQFQKELETLDDAKQNDICENLEASSDYCSALLKIDIFGPLEE 418
Db 360 EREAIEFPMKNSFDVDSQFQKELETLDDAKQNDICENLEASSDYCSALLKIDIFGPLEE 419
Qy 419 AVKQIYSPKGGHNLFIQKTBELKAKYRPRKGIQAEBVLQKYLKSKESVSHAILQPDQ 478
Db 420 EVAQEFYHKPGHKLFLQRMQKLNKANYRQPKGTQABEVLQTYLNKATVSRITLQTDQ 479
Qy 479 ALTEKTKKKAQVKAERAKAQAFLAIQONQEQMQRERLHQEQVQRMELAK----- 533
Db 480 VLTQKIQKKAQVKAERAKAQAFLAIQONQEQMQRERLHQEQVQRMELAK----- 533
Qy 534 -QNWLAEOQKMOE 545
Db 540 EQWILKQRAQEE 552

RESULT 8
Q8BU78 PRELIMINARY; PRT; 561 AA.
AC Q8BU78
AT Q8BU78
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched
DE library, clone:E03025M22 product:weakly similar to GUANYLATE BINDING
DE PROTEIN 5 (Fragment).
GN Name=Gbp5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6875(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/350555500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuura T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK087083; BAC39801.1; -
DR HSSP; P32455; IDG3.
DR MGD; MGI:2429943; Gbp5.
DR GO; GO:0005252; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001391; GBP.
DR Pfam; PF02263; GBP_1.
DR Pfam; PF02841; GBP_C; 1.
DR NON_TER 561 561
SQ SEQUENCE 561 AA; 63322 MW; 2C83B9838661FF39 CRC64;

Query Match 62.6%; Score 1905.5; DB 2; Length 561;
Best Local Similarity 69.0%; Pred. No. 1.6e-88;
Matches 380; Conservative 60; Mismatches 108; Indels 3; Gaps 2;

Qy 1 MALEIHSDMCLLENFNEQLKVNQEALEILSALTQPVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MAPEIHPEPLCLIGSTEGHLVTVNQEALKLSALTQPVVVAIVGLYRTGKSYLMNKLKAG 60
Qy 61 KNGGFSVASTVQSHTKGIWCVPHNPNNHTLVLLDTEGLGDEVEKADKNNDIOIFALAL 120
Db 61 KEKGFSVSTVQSHTKGIWCVPHNPNNHTLVLLDTEGLGDEVEKADKNNDIOIFALAI 120
Qy 121 LLSSTFVNTWKNIDQGAIDLHNVTELTDLTRKNSDSNQTEGEPAD-MSFFPDLVW 178
Db 121 LLSSTFVNTWKNIDQGAIDLHNVTELTDLTRKNSDSNQTEGEPAD-MSFFPDLVW 179
Qy 179 TLRDFCLGLEIDGQAVTTPDEYLENSLRPKQSDQDVQVNFNLRCLQKFFPKKCFIDL 238
Db 180 TLRDFCLDQANGHAITSDEYLENSLRPKQSDQDVQVNFNLRCLQKFFPKKCFVDA 239
Qy 239 PAHQKLAQLETLDPDELEPFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVITY 298
Db 240 PALGSKLSQLETLNNEELNSDFVQDLSEFCSHIFTQSKTKTLPGGIVNGPRLSLVITY 299
Qy 299 VNATSSGDLPCENAVLALAQRENSAAVQKAIAHYDQMGQKVOLPMETLOELDLHRTS 358
Db 300 VDAINSGLPSEIENVTLARRENSAAVQKAIAHYDQMSKQVLTPTTLOELDLHRTC 359
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QY 359 EREAIEVFMKNSGKVDQSFQKELETLLDAKQNDICRNLKLEASDYCSALLKDIQFGLPEE 418
Db 360 EREAIEIFRKHSPKDSGFEFFQKELESLLSAKQDEICKKNADASAALCSTLLGSIFKPLEQ 419
QY 419 AVKQGIYSPPGGHNLFIQTEBELKAKYREPRKGIQAEVLOKYLKSKESVSHAILQTDQ 478
Db 420 EVAQEFYHPPGGHKLFLQMEQLKANYRQPGKGTQAEVLTQYLNKAKETVSRITLQTDQ 479
QY 479 ALTETEKKKKAEQVKAEEAKAEQAORLAATORQNEQMMQERERLHOVQOMEIAQNWLA 538
Db 480 VLTDKEIQSKAQERAEARLEAQRLEAIRIOEQKKAEMERQHOQLRQIALEKARVAQ 539
QY 539 EQQKMOEQMQ 549
Db 540 EQQWILKQRAQ 550

RESULT 9
GBP2_HUMAN
ID -GBP2_HUMAN STANDARD; PRT; 591 AA.
AC P32456; Q86TB0.
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2)
DE (Guanine nucleotide-binding protein 2) (HuGBP-2).
GN Names=GBP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=91342675; PubMed=1715024;
RA Cheng Y.-S.E., Patterson C.E., Staeheli P.;
RT "Interferon-induced guanylate-binding proteins lack an N(7)KXD
RT consensus motif and bind GMP in addition to GDP and GTP.";
RL Mol. Cell. Biol. 11:4717-4725(1991).
RN [2]
RN REVISIONS.
RC TISSUE=Foreskin;
RA Schwemmler M.;
RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Fouscka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.-W., Weil B., Amid C., Fobo G., Han M., Osanger A.,
RA Wiemann S.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Binds GTP, GDP and GMP.
CC -!- INDUCTION: By interferon gamma during macrophage activation.
CC -!- SIMILARITY: Belongs to the GBP family.

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CC -----
CC EMBL; M55543; AAA67323.1; -
CC EMBL; AL832451; CAD89925.1; -
CC PIR; S70524; S70524.
CC HSSP; P32455; 1DG3.
CC Genem; HGNC:4183; GBP2.
CC H-InvDB; HIX0000764; -.
CC MIM; 600412; -.
CC GO; GO:0005525; F:GTP binding; TAS.
CC GO; GO:0006955; P:immune response; TAS.
CC InterPro; IPR003191; GBP.
CC Pfam; PF02263; GBP; 1.
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DR Pfam; PF02841; GBP_C; 1.
KW GTP-binding; Interferon induction; Lipoprotein; Multigene family;
KW Prenylation.
FT NP_BIND 45 52 GTP (By similarity).
FT NP_BIND 97 101 GTP (By similarity).
FT LIPID 588 598 S-geranylgeranyl cysteine (By
FT similarity).
FT CONFLICT 303 303 S -> G (in Ref. 3).
SQ SEQUENCE 591 AA; 67183 MW; E090809EE18FC8A8 CRC64;

Query Match 62.3%; Score 1897; DB 1; Length 591;
Best Local Similarity 63.5%; Pred. No. 4.6e-88;
Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;

QY 1 MALEIHMSPMCLIEFNEQKVNQBALEILSAITQPVVVVAIVGLYRTGKSLMKNLAG 60
Db 1 MAPEINLPGPMSLIIDNTKGQLVNPEALKILSAITQPVVVVAIVGLYRTGKSLMKNLAG 60
QY 61 KNGGFSVASTVQSHTKGIWICVPHNPWNHPTLVLLDTTEGLGDVEKADNKNDIQIPALAL 120
Db 61 KNGGFSLGSTVKSHTKGIWMCVPHPKKPEHTLVLLDTTEGLGDIEKGDNDNSWIFALAI 120
QY 121 LLSSTFVNTVTKIDQGAIDLHNTVELTDLKARNSPDLDRVEDPADSASFPPDLVWTL 180
Db 121 LLSSTFVNSMGTIINQAMDQLHYVTELTDRIKANSSPGNNSDVDSDAFVSFPFVWTL 180
QY 181 RPFCLGLEIDGOLVTPDEVLENSLRPKGSDORQVFNPLRCLIOKFFPKKCFIDFLPA 240
Db 181 RFTUELEVDPGPIITADDYLESLKRGTKDKSKSFNDPRLCIRKFFPKKCFVFDWFA 240
QY 241 HOKLAQLETLPPDELEPEFVQVTEFCYSIFSHSMTKTLPGGIMVNGSRLKNLVITYN 300
Db 241 PKKYLAHLQLEKEELNPDFIEQVAEFCYSILSHSNVKTLSGGIAVNGPRLSGLVITYN 300
QY 301 AISSGDLPCIEANAVIALAORENSAAVKIAIHYDQMGQKQVLPMTLOELDLHRTSR 360
Db 301 AISSGDLPCMENAVIALAQIENSAVAIAHYEQMGQKQVLPMTLOELDLHRTSR 360
QY 361 EAIEVFMKNSPKVDQSFQKELETLLDAKQNDICRNLKLEASDYCSALLKDIQFGLPEEAV 420
Db 361 EAIEVFMKNSFKVDQMFQKQLEAQRDDFCQNSKASSDCCWALLQDIFGPLEEDV 420
QY 421 KQGIYSKPGGHNLFIQKTEELKAKYREPRKGIQAEVLOKYLKSKESVSHAILQTDQAL 480
Db 421 KQGTFSKPGGYRLFTQKLELKNKYVQVPRKGIQAEVLOKYLKSKESVSHAILQTDQSL 480
QY 481 TTEKKKKAQVKAEEAKAEQAORLAATORQNEQMMQERERLHOVQOMEIAQNWLA 536
Db 481 SEKEAIEVERIKAESEAAKQMLEEIQKNEEMMEQKEKSYQEHVKQLTEKMERDAQL 540
QY 537 LAEQQ-----KMQEQMQVFINCFISPLPVTWVCSGSGKEGAARS CGSQGVW 585
Db 541 MAEQKTLALQEQE-----RLKKEGFENESKR---LQKDIW 575

RESULT 10
Q6GPH0
ID Q6GPH0 PRELIMINARY; PRT; 591 AA.
AC Q6GPH0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Guanylate binding protein 2, interferon-inducible.
GN Name=GBP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Smutcz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schmutz J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073163; AAH73163.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP; 1.
SQ SEQUENCE 591 AA; 67233 MW; 739CE562AF335776 CRC64;

Query Match 62.2%; Score 1892; DB 2; Length 591;
Best Local Similarity 63.5%; Pred. No. 8.2e-88;
Matches 377; Conservative 87; Mismatches 102; Indels 28; Gaps 4;

Qy 1 MALEIHMSDPMCLTENFEQKVNQAELEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MAPEINLPGRMSLDINTKQGLVWNPALKILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60

Qy 61 KNGFSAVSTVQSHTKGIWICVPHNPWNTLVLLDTEGLGDEYKADKNKDIQIFALAL 120
Db 61 KNGFSLGSTVKSHTKGIWICVPHNPWNTLVLLDTEGLGDEYKADKNKNDNDSWIFALAI 120

Qy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLRVEDPADSFFPDVWTL 180
Db 121 LLSSTFVYNSGTTINQAMDQVLYVTELTDLKARNSPGNNSVDSDADFVFFFAFWTL 180

Qy 181 RDCFLGLEIDQVTPDYEYLSRKPQGSQDQVQNFNPLRLCIQKFPFKKCFIDPLA 240
Db 181 RDCFLGLEIDQVTPDYEYLSRKPQGSQDQVQNFNPLRLCIQKFPFKKCFIDPLA 240

Qy 241 HQKLAQLETPDDELEPEFVQVTEFCSYIFSHMTKTLPGGIWNGSRKLNVLVTYN 300
Db 241 PKYLAHLEQKEBELNPDFTEQVAEFCSYIFLSHNVKTLSSGGIPVNGPRLESVLVTYN 300

Qy 301 AISSGDLPCIEAVNALAQAENSAAVQKAIHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCREAVNALAQAENSAAVQKAIHYDQMGQKQVQLPMETLQELLDLHRTSER 360

Qy 361 EAEVFMKNSFKVDQSQFQKELETLLDAKQNDIKCRNLEASSDYCSALLKIDIFGLEAV 420
Db 361 EAEVFMKNSFKVDQSQFQKELETLLDAKQNDIKCRNLEASSDYCSALLKIDIFGLEAV 420

Qy 421 KQGIYSKPGGHNLFIOKTEELKAKYPRKGIQAEVLYKYLKSKSVSHAIQTOAL 480
Db 421 KQGIYSKPGGHNLFIOKTEELKAKYPRKGIQAEVLYKYLKSKSVSHAIQTOAL 480

Qy 481 TETEKKEKAEQVAKAEKAEQVAKAEQVAKAEQVAKAEQVAKAEQVAKAEQVAKAEQV 536
Db 481 SEKEKAIEVERIKAEAEAKMLLEEIOKNEEMWQEKESYQSHVQKLTETKMERDRAQL 540

Qy 537 LAEQ-----KMQEQQMOVFINCFTISPLPVTNRVCSGKEGEAARSQSQGVW 585
Db 541 MAEQEKTALALQEQE-----RLKKEGFENESKR-----LQKDIW 575

RESULT 11
Q9H0R5 PRELIMINARY; PRT; 563 AA.
AC Q9H0R5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein DKFZp564C2478.
GN Name=DKFZp564C2478;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136680; CAB66615.1; -.
DR HSSP; P32455; 1DG3.
DR Genew; HGNC:4184; GBP3.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP; 1.
KW Hypothetical protein.
SQ SEQUENCE 563 AA; 64127 MW; 0C2FB7CE7FFCBCC3 CRC64;
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2].
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL EMBL: BC022272; AAH22272.1; -;
 DR HSSP; P32455; 1DC3.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro: IPR003191; GBP.
 DR Pfam; PF02263; GBP; 1.
 DR Pfam; PF02841; GBP; C; 1.
 SQ SEQUENCE 481 AA; 54034 MW; 2F8B6GBEA92EED87 CRC64;

 Query Match 58.0%; Score 1764; DB 2; Length 481;
 Best Local Similarity 71.1%; Pred. No. 1.9e-81;
 Matches 342; Conservative 64; Mismatches 75; Indels 0; Gaps 0;

 Qy 1 MALEIHMSDPMCLINFEQKLVNQEALEILSAITQPVVVAIVGLYRTGSKYLMNKLKAG 60
 Db 1 MAPEINLPQPSLIDNTKQGLVWNPPEALKILSAITQPVVVAIVGLYRTGSKYLMNKLKAG 60

 Qy 61 KNGFSVASTVQSHTKGIWICVPHNPVHTLVLLDTEGLGDEKADKNKNDIQIFALAL 120
 Db 61 KNGFSVASTVQSHTKGIWICVPHNPVHTLVLLDTEGLGDEKADKNKNDISWIFALAI 120

 Qy 121 LLSSTFVYNTVNTKIDQGAIDLLHNVTETLTLKARNSPDLRVEDPADSASFFPDVWTL 180
 Db 121 LLSSTFVYNSMGTTNQAMQDLHYVTELTDLKARNSPGNNSVDDSDAFVFFPAFWTL 180

 Qy 181 RDFCLGLEIDQVTPDEYLENSLRPKQSGDQVQNPNLPRLCIOKFPKKCFIDPLA 240
 Db 181 RDFCLEVDGEPIADDDYLESLKRLKGTDKSKSFNDPRLCIRKFPKCFKCFWOPA 240

 Qy 241 HQKLAOLETLPDDELEPEFVQVTEFCSYIFSHMTKTLPGGIMVNGSRKLNVLTYVN 300
 Db 241 PKYLAHLEQLKEELNPDFIEQVAEFCSYILSHSNVTKLSSGIPVNGPRLESILVLYVN 300

 Qy 301 AISSGDLPCINAVLALAQRENSAAVOKAIAHYDQOMGQKQVLPMPETLOELDLHRTSER 360
 Db 301 AISSGDLPCMENAVLALAQRENSAAVEAIAHYDQOMGQKQVLPMPETLOELDLHRTSER 360

 Qy 361 EAEIVFMKNSFKVDQSQFQKELETLLDAKNDICRNLEASSDYCSALLKDIQFPLEAV 420
 Db 361 EAEIVFMKNSFKVDQSQFQKLAQLEARDPCKQNSKASDCMALLQDIFGPLEEDV 420

 Qy 421 KQGYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQKLYSKESVSHAILQTOAL 480
 Db 421 KQGYTSKPGGVRLLFTQKLEQLKNKYYQVPRKGIQAEVLYQKLYSKESKEDVALLQTOQL 480

 Qy 481 T 481
 Db 481 S 481

 RESULT 14
 ID GBP2_RAT
 AC Q63663;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2)
 DE (Guanine nucleotide-binding protein 2) (p67).
 GN Name=Gbp2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1].
 RP SEQUENCE FROM N.A.; TISSUE SPECIFICITY, AND ISOPRENOID.
 RX MEDLINE=94198287; PubMed=8148370; DOI=10.1016/0167-4781(94)90284-4;
 RA Asundi V.K., Stahl R.C., Showalter L., Conner K.J., Carey D.J.;
 RT "Molecular cloning and characterization of an isoprenylated 67 kDa
 RT protein.";
 RL Biochim. Biophys. Acta 1217:257-265(1994).
 CC -!- FUNCTION: Binds GTP, GDP and GMP (By similarity).
 CC -!- TISSUE SPECIFICITY: Ubiquitous.
 CC -!- INDUCTION: By interferon gamma.
 CC -!- SIMILARITY: Belongs to the GBP family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M80367; AAA19909.1; ALT_INIT.
 DR PIR; S43506; S43506.
 DR HSSP; P32455; 1DC3.
 DR InterPro: IPR003191; GBP.
 DR Pfam; PF02263; GBP; 1.
 DR Pfam; PF02841; GBP; C; 1.
 DR GTP-binding; Interferon induction; Lipoprotein; Multigene family;
 KW Prenylation.
 FT NP_BIND 45 52 GTP (By similarity).
 FT NP_BIND 97 101 GTP (By similarity).
 FT LIPID 586 586 S-geranylgeranyl cysteine.
 SQ SEQUENCE 589 AA; 67109 MW; 5E52B79102C2D97F CRC64;

 Query Match 57.8%; Score 1757.5; DB 1; Length 589;
 Best Local Similarity 63.3%; Pred. No. 5.2e-81;
 Matches 346; Conservative 82; Mismatches 116; Indels 3; Gaps 1;

 Qy 1 MALEIHMSDPMCLINFEQKLVNQEALEILSAITQPVVVAIVGLYRTGSKYLMNKLKAG 60
 Db 1 MASBIHMLQPMCLIENTEAHLVINQEAIRILSAINQPVVVVAIVGLYRTGSKYLMNKLKAG 60

 Qy 61 KNGFSVASTVQSHTKGIWICVPHNPVHTLVLLDTEGLGDEKADKNKNDIQIFALAL 120
 Db 61 KRTGFSLGSTVQSHTKGIWICVPHNPVHTLVLLDTEGLGDEKADKNKNDICWIFALAL 120

 Qy 121 LLSSTFVYNTVNTKIDQGAIDLLHNVTETLTLKARNSPDLRVEDPADSASFFPDVWTL 180
 Db 121 LLSSTFVYNSMGTTNQAMQDLHYVTELTDLKSKSPDQSGIDDSANFVGFPTFWAL 180

 Qy 181 RDFCLGLEIDQVTPDEYLENSLRPKQSGDQVQNPNLPRLCIOKFPKKCFIDPLA 240
 Db 181 RDFSLELVNGKLVTPDEYLEHSLTLKKGADKTKSFNEPRLCIRKFPKCFKCFIDRPA 240

 Qy 241 HQKLAOLETLPDDELEPEFVQVTEFCSYIFSHMTKTLPGGIMVNGSRKLNVLTYVN 300
 Db 241 LRKQLCKLETGEBEELCEFEVQVAEFTSYIFSYSAVTKLGGIIVNGPRLSLVQTVVG 300

 Qy 301 AISSGDLPCINAVLALAQRENSAAVOKAIAHYDQOMGQKQVLPMPETLOELDLHRTSER 360
 Db 301 AISSGSLPCMESAVTLAQRENSAAVOKAIAHYEQMNQKIOMPTETLOELDLHRLIER 360

 Qy 361 EAEIVFMKNSFKVDQSQFQKELETLLDAKNDICRNLEASSDYCSALLKDIQFPLEAV 420
 Db 361 EAEIBIFLKNSPKVDQKQFQTELGNNLISKRDATFIKKNSDVSSAHCSDLIEDIFGPLEBEV 420

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Job time : 183 secs

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